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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:47:27 ; Search time 23 Seconds  
(without alignments)  
707.543 Million cell updates/sec

Title: US-10-694-978-4

Perfect score: 218

Sequence: 1 MSFVGNSGVKMGSEDEK.....IEFSFQPVCKAEMSPSEVSD 218

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 6

Total number of hits satisfying chosen parameters: 652

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:\*

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	218	100.0	218	4	US-09-398-412B-4
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4	129	59.2	167	3	US-09-128-155-7
5	129	59.2	178	3	US-09-128-155-2
6	115	52.8	115	3	US-09-128-155-5
7	115	52.8	115	3	US-09-128-155-9
8	115	52.8	115	3	US-09-128-155-13
9	55	25.2	218	4	US-09-398-412B-2
10	52	23.9	185	3	US-09-128-155-18
11	30	13.8	63	3	US-09-128-155-4
12	19	8.7	52	3	US-09-128-155-8
13	14	6.4	21	3	US-09-128-155-12
14	8	3.7	559	4	US-09-364-206-47
15	8	3.7	651	3	US-08-650-766-6
16	8	3.7	651	3	US-09-922-635-5
17	8	3.7	651	4	US-09-389-487-5
18	8	3.7	1070	3	US-08-922-635-22
19	8	3.7	1504	4	US-09-364-206-2
20	8	3.7	1622	3	US-08-972-927-6
21	7	3.2	61	4	US-09-248-796A-26517
22	7	3.2	73	4	US-09-107-532A-6620
23	7	3.2	108	4	US-09-513-999C-5928
24	7	3.2	148	4	US-09-640-211A-790
25	7	3.2	254	4	US-09-796-149B-4
26	7	3.2	259	4	US-09-540-236-2112
27	7	3.2	264	4	US-09-107-532A-7009

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102	6	2.8	93	4	US-09-248-796A-26322	Sequence 26322, A	175	6	2.8	177	4	US-09-893-737-30	Sequence 30, Appl
103	6	2.8	94	4	US-09-949-016-10599	Sequence 10599, A	176	6	2.8	178	1	US-08-825-891-1	Sequence 1, Appli
104	6	2.8	99	4	US-09-540-236-2992	Sequence 2992, Ap	177	6	2.8	180	4	US-09-270-767-31695	Sequence 31695, A
105	6	2.8	104	4	US-09-230-485-9	Sequence 9, Appli	178	6	2.8	180	4	US-09-270-767-46912	Sequence 46912, A
106	6	2.8	104	4	US-09-513-999C-6549	Sequence 6549, Ap	179	6	2.8	182	4	US-09-904-615-114	Sequence 114, App
107	6	2.8	104	4	US-09-640-211A-711	Sequence 711, App	180	6	2.8	183	4	US-09-621-976-3942	Sequence 3942, Ap
108	6	2.8	105	4	US-09-583-110-4875	Sequence 4875, Ap	181	6	2.8	184	4	US-09-938-391A-11	Sequence 11, Appl
109	6	2.8	106	3	US-09-199-637A-283	Sequence 283, App	182	6	2.8	186	4	US-09-328-352-4727	Sequence 4727, Ap
110	6	2.8	111	4	US-09-270-767-61594	Sequence 61594, A	183	6	2.8	188	4	US-09-134-000C-6806	Sequence 6806, Ap
111	6	2.8	113	4	US-09-513-999C-4899	Sequence 4899, Ap	184	6	2.8	189	4	US-09-134-000C-5580	Sequence 5580, Ap
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115	6	2.8	118	4	US-09-765-815-8	Sequence 8, Appli	188	6	2.8	195	4	US-09-252-991A-27353	Sequence 27353, A
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118	6	2.8	122	4	US-09-461-325-355	Sequence 355, App	191	6	2.8	196	4	US-10-274-978-17	Sequence 17, Appl
119	6	2.8	122	4	US-10-012-542-355	Sequence 355, App	192	6	2.8	196	4	US-10-697-263-17	Sequence 17, Appl
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121	6	2.8	122	4	US-09-902-540-11364	Sequence 11364, A	194	6	2.8	197	4	US-09-107-532A-6657	Sequence 6657, Ap
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126	6	2.8	139	4	US-09-252-991A-21467	Sequence 21467, A	199	6	2.8	209	4	US-09-904-615-168	Sequence 168, App
127	6	2.8	139	4	US-09-252-991A-24681	Sequence 24681, A	200	6	2.8	209	4	US-08-778-717-7	Sequence 7, Appli
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158	6	2.8	152	4	US-09-205-258-564	Sequence 564, App	231	6	2.8	240	4	US-09-270-767-40542	Sequence 40542, A
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254	6	2.8	280	4	US-09-711-164-468	Sequence 468, App	327	6	382	4	US-09-560-761B-14	Sequence 14, Appl
255	6	2.8	280	4	US-10-101-464A-621	Sequence 621, App	328	6	385	4	US-09-270-767-32506	Sequence 32506, A
256	6	2.8	281	4	US-09-134-000C-4462	Sequence 4462, Ap	329	6	385	4	US-09-270-767-47723	Sequence 47723, A
257	6	2.8	289	4	US-09-489-039A-7935	Sequence 7935, Ap	330	6	391	4	US-09-583-110-3765	Sequence 3765, Ap
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297	6	2.8	346	3	US-08-459-595A-19	Sequence 19, Appl	370	6	443	4	US-09-273-871A-5	Sequence 5, Appl
298	6	2.8	346	3	US-08-459-504B-19	Sequence 19, Appl	371	6	443	4	US-09-482-558A-30	Sequence 30, Appl
299	6	2.8	346	3	US-08-459-444A-19	Sequence 19, Appl	372	6	443	4	US-10-083-452-5	Sequence 5, Appl
300	6	2.8	346	3	US-09-547-422-19	Sequence 19, Appl	373	6	444	4	US-09-129-668-8	Sequence 8, Appl
301	6	2.8	346	4	US-09-988-462-19	Sequence 19, Appl	374	6	445	4	US-09-107-532A-5506	Sequence 5506, Ap
302	6	2.8	346	4	US-09-248-796A-16202	Sequence 16202, A	375	6	445	4	US-08-861-990-11	Sequence 11, Appl
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304	6	2.8	348	3	US-09-203-716-3	Sequence 3, Appl	377	6	446	3	US-09-457-046B-74	Sequence 74, Appl
305	6	2.8	348	3	US-09-684-254-3	Sequence 3, Appl	378	6	446	4	US-09-270-767-61103	Sequence 61103, A
306	6	2.8	348	4	US-09-409-926-3	Sequence 3, Appl	379	6	446	4	US-09-866-570B-74	Sequence 74, Appl
307	6	2.8	350	4	US-09-270-767-43557	Sequence 43557, A	380	6	447	4	US-09-394-142B-24	Sequence 24, Appl
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310	6	2.8	358	4	US-09-489-039A-12539	Sequence 12539, A	383	6	452	4	US-09-252-991A-19099	Sequence 19099, A
311	6	2.8	360	4	US-09-270-767-44963	Sequence 44963, A	384	6	454	3	US-09-092-315-8	Sequence 8, Appl
312	6	2.8	362	4	US-09-291-299A-6	Sequence 6, Appl	385	6	454	4	US-09-733-524A-8	Sequence 8, Appl
313	6	2.8	368	4	US-09-252-991A-26170	Sequence 26170, A	386	6	455	4	US-09-711-164-416	Sequence 416, App
314	6	2.8	369	4	US-09-252-991A-24423	Sequence 24423, A	387	6	458	1	US-08-112-817C-2	Sequence 2, Appl
315	6	2.8	370	4	US-09-252-991A-24608	Sequence 24608, A	388	6	458	4	US-09-694-519-5	Sequence 5, Appl
316	6	2.8	376	4	US-09-252-991A-30994	Sequence 30994, A	389	6	458	4	US-09-694-519-7	Sequence 7, Appl
317	6	2.8	376	4	US-09-248-796A-14887	Sequence 14887, A	390	6	464	3	US-08-957-063-6	Sequence 6, Appl
318	6	2.8	377	1	US-08-153-848-42	Sequence 42, Appl	391	6	464	3	US-09-487-685-6	Sequence 6, Appl
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395	6	2.8	464	4	US-09-388-116C-6	Sequence 6, Appli	468	6	2.8	637	4	US-09-390-224-4	Sequence 4, Appli
396	6	2.8	470	4	US-09-291-299A-1	Sequence 1, Appli	469	6	2.8	640	4	US-09-328-352-8058	Sequence 8058, Ap
397	6	2.8	476	3	US-09-092-315-5	Sequence 5, Appli	470	6	2.8	643	4	US-09-949-016-10897	Sequence 10897, A
398	6	2.8	476	4	US-09-733-524A-5	Sequence 5, Appli	471	6	2.8	643	4	US-09-949-016-10903	Sequence 10903, A
399	6	2.8	476	4	US-09-291-299A-3	Sequence 3, Appli	472	6	2.8	645	4	US-09-248-796A-20288	Sequence 20288, A
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402	6	2.8	486	3	US-09-092-315-2	Sequence 2, Appli	475	6	2.8	664	3	US-08-957-063-18	Sequence 18, Appl
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414	6	2.8	508	4	US-08-781-986A-5241	Sequence 5241, Ap	487	6	2.8	716	3	US-08-818-823-4	Sequence 4, Appli
415	6	2.8	510	3	US-09-134-001C-4541	Sequence 4541, Ap	488	6	2.8	716	3	US-09-037-190-38	Sequence 38, Appl
416	6	2.8	511	4	US-09-252-991A-18691	Sequence 18691, A	489	6	2.8	716	3	US-09-037-190-46	Sequence 46, Appl
417	6	2.8	513	4	US-09-252-991A-32774	Sequence 32774, A	490	6	2.8	716	3	US-09-037-192-38	Sequence 38, Appl
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425	6	2.8	532	4	US-09-489-039A-10011	Sequence 10011, A	498	6	2.8	716	3	US-09-338-128A-38	Sequence 38, Appl
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428	6	2.8	533	4	US-09-546-013-21	Sequence 21, Appl	501	6	2.8	716	3	US-09-232-346-46	Sequence 46, Appl
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430	6	2.8	533	6	5206152-2	Patent No. 5206152	503	6	2.8	716	5	PCT-US94-07297-37	Sequence 37, Appl
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434	6	2.8	548	3	US-08-687-590-31	Sequence 31, Appl	507	6	2.8	725	4	US-09-902-540-16658	Sequence 16658, A
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439	6	2.8	556	4	US-09-438-185A-210	Sequence 210, App	512	6	2.8	739	4	US-10-202-619-2	Sequence 2, Appli
440	6	2.8	558	4	US-09-540-236-2943	Sequence 2943, Ap	513	6	2.8	744	3	US-09-328-352-7920	Sequence 7920, Ap
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442	6	2.8	567	4	US-09-733-728A-2	Sequence 2, Appli	515	6	2.8	747	4	US-09-902-540-10542	Sequence 10542, A
443	6	2.8	575	4	US-09-248-796A-15765	Sequence 15765, A	516	6	2.8	747	4	US-09-252-991A-27424	Sequence 27424, A
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446	6	2.8	577	4	US-09-248-796A-18822	Sequence 18822, A	519	6	2.8	762	2	US-08-907-166-10	Sequence 10, Appl
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448	6	2.8	580	4	US-09-129-668-1	Sequence 1, Appli	521	6	2.8	762	4	US-09-724-653-7	Sequence 7, Appli
449	6	2.8	582	3	US-08-906-865-3	Sequence 3, Appli	522	6	2.8	764	4	US-09-370-838-67	Sequence 67, Appl
450	6	2.8	582	4	US-09-129-668-3	Sequence 3, Appli	523	6	2.8	764	4	US-09-538-092-944	Sequence 944, App
451	6	2.8	587	4	US-09-902-540-15496	Sequence 15496, A	524	6	2.8	764	4	US-09-854-133-67	Sequence 67, Appl
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453	6	2.8	591	4	US-09-688-188B-103	Sequence 103, App	526	6	2.8	766	4	US-09-724-653-15	Sequence 15, Appl
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548	6	2.8	823	4	US-09-949-016-6852	Sequence 6852, Ap	621	6	2.8	2201	4	US-09-539-601-15	Sequence 15, Appli
549	6	2.8	824	4	US-09-134-000C-4908	Sequence 4908, Ap	622	6	2.8	2201	4	US-10-029-907-3	Sequence 3, Appli
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551	6	2.8	833	4	US-09-252-991A-25227	Sequence 25227, A	624	6	2.8	2472	4	US-09-538-092-1312	Sequence 1312, Ap
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565	6	2.8	921	4	US-09-699-266A-9	Sequence 9, Appli	638	6	2.8	2843	3	US-08-450-582-2	Sequence 2, Appli
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567	6	2.8	934	4	US-09-949-016-7286	Sequence 7286, Ap	640	6	2.8	2843	4	US-08-449-731-2	Sequence 2, Appli
568	6	2.8	942	4	US-09-254-776B-51	Sequence 51, Appli	641	6	2.8	2843	4	US-10-092-138A-30	Sequence 30, Appli
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572	6	2.8	1000	4	US-09-187-330-1	Sequence 1, Appli	645	6	2.8	2973	3	US-09-136-605-7	Sequence 7, Appli
573	6	2.8	1076	4	US-09-949-016-6610	Sequence 6610, Ap	646	6	2.8	3010	4	US-09-539-601-3	Sequence 3, Appli
574	6	2.8	1077	4	US-09-412-210-1	Sequence 1, Appli	647	6	2.8	3010	4	US-09-539-601-21	Sequence 21, Appli
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576	6	2.8	1085	4	US-09-095-881-2	Sequence 2, Appli	649	6	2.8	3010	4	US-09-539-601-33	Sequence 33, Appli
577	6	2.8	1089	4	US-09-248-796A-19072	Sequence 19072, A	650	6	2.8	3169	3	US-09-453-702B-257	Sequence 257, App
578	6	2.8	1095	4	US-09-555-554-4	Sequence 4, Appli	651	6	2.8	3913	4	US-09-949-016-10933	Sequence 10933, A
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582	6	2.8	1116	4	US-09-252-991A-32442	Sequence 32442, A							
583	6	2.8	1130	4	US-09-538-092-834	Sequence 834, App							
584	6	2.8	1140	2	US-08-657-641-7	Sequence 7, Appli							
585	6	2.8	1140	5	PCT-US94-07233-7	Sequence 7, Appli							
586	6	2.8	1148	4	US-09-949-016-6798	Sequence 6798, Ap							
587	6	2.8	1164	4	US-09-949-016-9269	Sequence 9269, Ap							
588	6	2.8	1169	4	US-09-949-016-9630	Sequence 9630, Ap							
589	6	2.8	1192	4	US-09-902-540-12662	Sequence 12662, A							
590	6	2.8	1203	3	US-09-351-200-2	Sequence 2, Appli							
591	6	2.8	1217	4	US-09-949-016-7454	Sequence 7454, Ap							
592	6	2.8	1237	1	US-08-241-853-2	Sequence 2, Appli							
593	6	2.8	1237	2	US-08-850-917-2	Sequence 2, Appli							
594	6	2.8	1278	4	US-09-902-540-16646	Sequence 16646, A							
595	6	2.8	1289	4	US-09-949-016-7313	Sequence 7313, Ap							
596	6	2.8	1342	4	US-09-561-709B-13	Sequence 13, Appli							
597	6	2.8	1427	4	US-09-538-092-1044	Sequence 1044, Ap							
598	6	2.8	1463	4	US-09-949-016-11696	Sequence 11696, A							
599	6	2.8	1464	3	US-08-891-640-2	Sequence 2, Appli							
600	6	2.8	1464	4	US-09-949-016-6738	Sequence 6738, Ap							
601	6	2.8	1564	4	US-09-976-594-309	Sequence 309, App							
602	6	2.8	1596	4	US-09-538-092-887	Sequence 887, App							
603	6	2.8	1621	3	US-08-972-927-3	Sequence 3, Appli							
604	6	2.8	1622	4	US-09-231-899-72	Sequence 72, Appli							
605	6	2.8	1665	4	US-09-858-664A-2	Sequence 2, Appli							
606	6	2.8	1665	4	US-10-274-978-2	Sequence 2, Appli							
607	6	2.8	1665	4	US-10-657-263-2	Sequence 2, Appli							
608	6	2.8	1724	4	US-09-607-510-2	Sequence 2, Appli							
609	6	2.8	1857	4	US-09-917-254-91	Sequence 91, Appli							
610	6	2.8	1938	4	US-09-949-016-6417	Sequence 6417, Ap							
611	6	2.8	1959	4	US-09-949-016-8134	Sequence 8134, Ap							

## ALIGNMENTS

## RESULT 1

US-09-398-412B-4  
; Sequence 4, Application US/09398412B  
; Patent No. 6680380

; GENERAL INFORMATION:  
; APPLICANT: Titanis, Jacqueline C.  
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-lzeta, related reage

; TITLE OF INVENTION: methods

; FILE REFERENCE: DX0904K

; CURRENT APPLICATION NUMBER: US/09/398,412B

; CURRENT FILING DATE: 1999-09-17

; PRIOR FILING DATE: 1998-09-18

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 218

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-398-412B-4

Query Match 100.0%; Score 218; DB 4; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.5e-212;

Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 MSFVGENSGVKGSEDWEKDEPQCCLEDPVSLPAMNFVHTSPKVNLPKPF 60  
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Db      1  MSFVGENSGVMKGSDEWKDEPOCCLEDPAVSPLEPGPSLPAMNFVHTSPVKNLNPKKF 60
Qy      61 SIHQDHKVLVLDGSLNIAPVDKNYIRPEIFFALASSLSASAEKSGSPILLGVSKGEFCL 120
Db      61 SIHQDHKVLVLDGSLNIAPVDKNYIRPEIFFALASSLSASAEKSGSPILLGVSKGEFCL 120
Qy     121 YCDKDKGQSHPSLQKKEKMLKLAQAOKESARRPFIFYRAQVGSNNMLESAAHPGWFTCTS 180
Db     121 YCDKDKGQSHPSLQKKEKMLKLAQAOKESARRPFIFYRAQVGSNNMLESAAHPGWFTCTS 180
Qy     181 CNCNEPVGVTDFENRKHIEFSFPVCKAEMSPSEVSD 218
Db     181 CNCNEPVGVTDFENRKHIEFSFPVCKAEMSPSEVSD 218

* RESULT 2
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293,625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match      80.7%; Score 176; DB 3; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.9e-170;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      43 MNFVHTSPVKNLNPKKFSIHDQHKVLVLDGSLNIAPVDKNYIRPEIFFALASSLSAS 102
Db      43 MNFVHTSPVKNLNPKKFSIHDQHKVLVLDGSLNIAPVDKNYIRPEIFFALASSLSAS 102
Qy     103 AEKGSPIILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKESARRPFIFYRAQVG 162
Db     103 AEKGSPIILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKESARRPFIFYRAQVG 162
Qy     163 SNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKAEMSPSEVSD 218
Db     163 SNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKAEMSPSEVSD 218

RESULT 3
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

Query Match      59.2%; Score 129; DB 3; Length 136;
Best Local Similarity 100.0%; Pred. No. 1.2e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      90 IFFALASSLSASAEKSGSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKES 149
Db      90 IFFALASSLSASAEKSGSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKES 149
Qy     150 ARRPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKA 209
Db     150 ARRPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKA 209
Qy     210 EMSPSEVSD 218
Db     210 EMSPSEVSD 136

RESULT 4
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-7

Query Match      59.2%; Score 129; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.4e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      90 IFFALASSLSASAEKSGSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKES 149
Db      90 IFFALASSLSASAEKSGSPILLGVSKGEFCLYCDKDKGQSHPSLQKKEKMLKLAQAOKES 98
Qy     150 ARRPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKA 209
Db     150 ARRPFFIFYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDFENRKHIEFSFPVCKA 158
Qy     210 EMSPSEVSD 218
Db     210 EMSPSEVSD 167

RESULT 5
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

Query Match          59.2%; Score 129; DB 3; Length 178;
Best Local Similarity 100.0%; Pred. No. 1.5e-122;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 IFFALASSLSASAEKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKES 149
Db 50 IFFALASSLSASAEKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKES 109

Qy 150 ARRPFIYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKA 209
Db 110 ARRPFIYRAQVGSNNMLESAAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKA 169

Qy 210 EMPSPSEVSD 218
Db 170 EMPSPSEVSD 178

RESULT 6
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

Query Match          52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db 1 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy 164 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 218
Db 61 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 115

RESULT 7
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
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; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-9

Query Match          52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db 1 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy 164 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 218
Db 61 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 115

RESULT 8
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-13

Query Match          52.8%; Score 115; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.5e-108;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 163
Db 1 EKSPILLGVSKGEFCLYCDKDGQSHPSLQKKEKLMKLAQKESARRPPFIYRAQVGS 60

Qy 164 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 218
Db 61 WNMLESAHPGWFTCTSCNCNEPVGVTDKFENRKHIEFSPQVCKAEMSPSEVSD 115

RESULT 9
US-09-398-412B-2
; Sequence 2, Application US/09398412B
; Patent No. 6680380
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage
; FILE REFERENCE: DX0904K
; CURRENT APPLICATION NUMBER: US/09/398,412B
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: US 60/100948
; PRIOR FILING DATE: 1998-09-18
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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-398-412B-2

Query Match      25.2%; Score 55; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 109 ILLGVSGEFLCYCDKDGQSHPSLQIKKELMKLAQKESARRPFIYRAQVGS 163
Db 109 ILLGVSGEFLCYCDKDGQSHPSLQIKKELMKLAQKESARRPFIYRAQVGS 163

RESULT 10
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: synthetically generated
; LOCATION: (1)...(185)
; OTHER INFORMATION: human sequence predicted using an alignment algorithm which
; OTHER INFORMATION: predicts presence of alternatively spliced exons for a protein of
; OTHER INFORMATION: interest in a stretch of genomic DNA
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(185)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-128-155-18

Query Match      23.9%; Score 52; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 KEKLMKLAQKESARRPFIYRAQVGSNNMLESAAHPGWFICTSCNCEPVG 188
Db 113 KEKLMKLAQKESARRPFIYRAQVGSNNMLESAAHPGWFICTSCNCEPVG 164

RESULT 11
US-09-128-155-4
; Sequence 4, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
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; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-4

Query Match      13.8%; Score 30; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 9.3e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSFVGNSGVKMGSEDEWKEDEPQCLEDPA 30
Db 1 MSFVGNSGVKMGSEDEWKEDEPQCLEDPA 30

RESULT 12
US-09-128-155-8
; Sequence 8, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-8

Query Match      8.7%; Score 19; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 MGSEDEWKEDEPQCLEDPA 30
Db 1 MGSEDEWKEDEPQCLEDPA 19

RESULT 13
US-09-128-155-12
; Sequence 12, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-12
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Query Match 6.4%; Score 14; DB 3; Length 21;  
Best Local Similarity 100.0%; Pred. No. 5.3e-07;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Search completed: October 13, 2005, 18:55:15  
Job time : 35 secs

Qy 90 IFFALASSLSASA 103  
| | | | | | | | | |  
Db 8 IFFALASSLSASA 21

RESULT 14  
US-09-364-206-47  
; Sequence 47, Application US/09364206  
; Patent No. 6475752  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Baugh, Mariah R.  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: Mammalian Imidazoline Receptor  
; FILE REFERENCE: PC-0006 US  
; CURRENT APPLICATION NUMBER: US/09/364,206  
; CURRENT FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: PERL Program  
; SEQ ID NO 47  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY:  
; OTHER INFORMATION: W43396  
; PUBLICATION INFORMATION:  
US-09-364-206-47

Query Match 3.7%; Score 8; DB 4; Length 559;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
| | | | | | | | | |  
Db 106 ALASSLS 113

RESULT 15  
US-08-650-766-6  
; Sequence 6, Application US/08650766D  
; Patent No. 6015690  
; GENERAL INFORMATION:  
; APPLICANT: PILETZ, John E.  
; APPLICANT: IVANOV, Tina R.  
; TITLE OF INVENTION: DNA SEQUENCE ENCODING A HUMAN IMIDAZOLINE RECEPTOR AND  
; TITLE OF INVENTION: METHOD FOR CLONING THE SAME  
; FILE REFERENCE: Corrected Sequence Listing  
; Patent No. 6015690  
; CURRENT APPLICATION NUMBER: US/08/650,766D  
; CURRENT FILING DATE: 1996-05-20  
; EARLIER APPLICATION NUMBER: US 60/012,600  
; EARLIER FILING DATE: 1996-03-01  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 651  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-650-766-6

Query Match 3.7%; Score 8; DB 3; Length 651;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100  
| | | | | | | | | |  
Db 106 ALASSLS 113

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OM protein - protein search, using sw model

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634.280 Million cell updates/sec

Title: US-10-694-978-4

Perfect score: 218

Sequence: 1 MSFVGENSGVMGSEDWEK.....IEFSFQPVCKAEMSPSEVSD 218

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Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	80.7	218	1	11F7_HUMAN
2	55	25.2	219	2	Q7RU00
3	9	4.1	196	2	Q97CB6
4	8	3.7	197	2	Q9SAQ1
5	8	3.7	161	2	Q8ZQ12
6	8	3.7	234	2	Q87JK9
7	8	3.7	256	2	Q72ME6
8	8	3.7	256	2	Q8EY26
9	8	3.7	267	2	Q73909
10	8	3.7	341	1	LP5L_RHIME
11	8	3.7	412	1	P0K4_MOUSE
12	8	3.7	413	2	Q9YCD8
13	8	3.7	595	2	Q9UEU4
14	8	3.7	787	2	Q8RX76
15	8	3.7	931	2	Q7SE30
16	8	3.7	982	2	Q65833
17	8	3.7	982	2	Q93Y68
18	8	3.7	993	2	Q7L8M3
19	8	3.7	1354	2	Q9EPW8
20	8	3.7	1427	1	ABC1_SCHPO
21	8	3.7	1480	2	Q80TM9
22	8	3.7	1504	2	Q8PGP3
23	8	3.7	1504	2	Q6PIB4
24	8	3.7	1504	2	Q722X6
25	8	3.7	1504	2	Q9UE36
26	8	3.7	1528	2	Q9Y211
27	8	3.7	1622	2	Q24635
28	8	3.7	1622	2	Q9C8G9
29	8	3.7	2118	2	Q76904
30	7	3.2	55	2	Q6QW36
31	7	3.2	73	2	Q8HXG7

32	7	3.2	88	2	Q8IGB4	Q81ge4 drosophila
33	7	3.2	89	2	Q8LC91	Q81c91 arabidopsis
34	7	3.2	91	2	Q86H93	Q86h93 dictyosteli
35	7	3.2	98	2	Q7Q5G1	Q7q5g1 anopheles g
36	7	3.2	99	2	Q6UXS1	Q6uxs1 homo sapien
37	7	3.2	107	2	Q9GXD7	Q9gyd7 leishmania
38	7	3.2	116	2	Q9YA88	Q9ya88 aeropyrum p
39	7	3.2	118	2	Q9MZQ7	Q9mzq7 lepus towns
40	7	3.2	118	2	Q9MZQ8	Q9mzq8 lepus calif
41	7	3.2	120	2	Q8R1S5	Q8r1s5 mus musculu
42	7	3.2	124	2	Q83XD6	Q83xd6 xanthomonas
43	7	3.2	130	2	Q9YXR6	Q9y9r6 aeropyrum p
44	7	3.2	131	2	Q8C339	Q8c339 mus musculu
45	7	3.2	132	2	Q9C9P6	Q9c9p6 arabidopsis
46	7	3.2	133	2	Q59454	Q59454 pyrococcus
47	7	3.2	134	1	Y605_METJA	Q58022 methanococc
48	7	3.2	134	2	Q6ZSD3	Q6zed3 homo sapien
49	7	3.2	135	2	Q70MM1	Q70mm1 crasseotrea
50	7	3.2	145	2	Q9MZQ5	Q9mzq5 oryctolagus
51	7	3.2	145	2	Q8C383	Q8c383 mus musculu
52	7	3.2	173	2	Q6M9B0	Q6m9b0 neurospora
53	7	3.2	177	2	Q7PMC0	Q7pmc0 anopheles g
54	7	3.2	181	2	Q9NF98	Q9nf98 plasmodium
55	7	3.2	182	2	Q9PSV8	Q9p5v8 neurospora
56	7	3.2	185	2	Q7RVZ3	Q7rvz3 neurospora
57	7	3.2	197	2	Q6ZTI9	Q6zti9 homo sapien
58	7	3.2	206	2	Q89MZ6	Q89mz6 bradyrhizob
59	7	3.2	208	1	RR9_ARATH	Q9xj27 arabidopsis
60	7	3.2	208	2	Q67Y29	Q67y29 arabidopsis
61	7	3.2	208	2	Q681V1	Q681v1 arabidopsis
62	7	3.2	217	2	Q8C4F8	Q8c4f8 mus musculu
63	7	3.2	223	2	Q72YM4	Q72ym4 bacillus ce
64	7	3.2	223	2	Q6AQZ9	Q6aqz9 desulfotale
65	7	3.2	240	2	Q9KFO9	Q9kfg9 bacillus ha
66	7	3.2	241	2	Q9MZB1	Q9mzr1 oryctolagus
67	7	3.2	257	2	Q64S01	Q64sh1 bacteroides
68	7	3.2	263	2	Q821H3	Q821h3 chlamydomo
69	7	3.2	265	2	Q9YTM3	Q9ytm3 ateline her
70	7	3.2	271	1	RRF_SPIOL	P82231 spinacia ol
71	7	3.2	275	2	Q6FX56	Q6fx56 candida gla
72	7	3.2	275	2	Q8S5P7	Q8s5p7 oryza sativ
73	7	3.2	276	2	Q7XB79	Q7xb79 oryza sativ
74	7	3.2	277	2	O24686	O24686 bacillus su
75	7	3.2	279	1	LGT_STAAH	P60961 staphylococ
76	7	3.2	279	1	LGT_STAAH	P60962 staphylococ
77	7	3.2	279	1	LGT_STAAU	P60963 staphylococ
78	7	3.2	279	1	LGT_STAAW	Q8nx18 staphylococ
79	7	3.2	279	2	Q6GB69	Q6gb69 staphylococ
80	7	3.2	280	2	Q6GIN0	Q6gin0 staphylococ
81	7	3.2	283	1	AROE_XANAC	Q9pfe9 xanthomonas
82	7	3.2	283	2	Q9L539	Q9l539 xanthomonas
83	7	3.2	284	2	Q6TV51	Q6tv51 bacillus me
84	7	3.2	290	1	OXAA_STAAH	P85628 staphylococ
85	7	3.2	290	1	OXAA_STAAH	P85629 staphylococ
86	7	3.2	290	1	OXAA_STAAW	P85630 staphylococ
87	7	3.2	290	2	Q6G7M0	Q6g7m0 staphylococ
88	7	3.2	290	2	Q6GEY5	Q6gey5 staphylococ
89	7	3.2	291	2	Q8LQ63	Q8lq63 oryza sativ
90	7	3.2	293	2	Q8XWT4	Q8xwt4 raistonia s
91	7	3.2	295	2	Q7VSV0	Q7vsv0 bordetella
92	7	3.2	295	2	Q7W3R3	Q7w3r3 bordetella
93	7	3.2	295	2	Q7WF41	Q7wf41 bordetella
94	7	3.2	297	2	Q89GH7	Q89gh7 bradyrhizob
95	7	3.2	301	2	O17553	O17553 caenorhabdi
96	7	3.2	303	2	O06849	O06849 rhodobacter
97	7	3.2	307	2	O34780	O34780 bacillus su
98	7	3.2	309	1	O5AT_HUMAN	Q8nhc5 homo sapien
99	7	3.2	317	2	Q755P3	Q755p3 ashbya gos
100	7	3.2	321	2	Q7RNE6	Q7rne6 plasmodium
101	7	3.2	322	2	Q7VAR7	Q7var7 prochloroco
102	7	3.2	326	1	NU37_HUMAN	Q8nfh4 homo sapien
103	7	3.2	326	1	NU37_MOUSE	Q9cwu9 mus musculu
104	7	3.2	326	2	Q9L8N6	Q9l8n6 haemophilus

105	7	3.2	326	2	Q9CZ80	Q9CZ80 m. mus muscu	178	7	3.2	485	2	Q8M9F1	Q8m9f1 luzula mult
106	7	3.2	329	2	Q7UEV0	Q7uev0 rhodopirell	179	7	3.2	492	2	Q7RZ74	Q7rz74 neurospora
107	7	3.2	332	2	Q72QP9	Q72qp9 leptospira	180	7	3.2	502	2	Q64IW9	Q64iw9 fundulus he
108	7	3.2	332	2	Q8F5E2	Q8f5e2 leptospira	181	7	3.2	505	2	Q98QG8	Q98qg8 rhizobium l
109	7	3.2	335	2	Q648E6	Q648e6 uncultured	182	7	3.2	505	2	Q64IX0	Q64ix0 fundulus he
110	7	3.2	335	2	Q72P82	Q72pe2 leptospira	183	7	3.2	516	2	Q6K975	Q6k975 oryza sativ
111	7	3.2	335	2	Q8CVF2	Q8cvf2 leptospira	184	7	3.2	520	2	Q6H4F1	Q6h4f1 oryza sativ
112	7	3.2	338	2	Q6IF96	Q6if96 homo sapien	185	7	3.2	521	2	Q74DZ3	Q74dz3 geobacter s
113	7	3.2	353	2	Q68DY6	Q68dy6 homo sapien	186	7	3.2	526	2	Q6MIC6	Q6mic6 dellolovibri
114	7	3.2	366	2	Q23103	Q23103 caenorhabdi	187	7	3.2	532	2	Q65DE0	Q65de0 bacillus li
115	7	3.2	366	2	Q7V671	Q7v671 prochloroco	188	7	3.2	540	2	Q8GX33	Q8gx33 arabidopsis
116	7	3.2	369	2	Q6TAB5	Q6tab5 symbiont ba	189	7	3.2	541	2	P89039	P89039 la piedad-m
117	7	3.2	372	2	Q6ZPH0	Q6zph0 mus musculu	190	7	3.2	547	2	Q64IX2	Q64ix2 fundulus he
118	7	3.2	373	2	Q8VNT7	Q8vnt7 enterobacte	191	7	3.2	560	2	Q7WX30	Q7wx30 alcaigenes
119	7	3.2	376	2	Q8HDC3	Q8hdg3 pediastrum	192	7	3.2	573	2	Q9X141	Q9x141 arabidopsis
120	7	3.2	377	1	CYCI_HUMAN	Q14094 homo sapien	193	7	3.2	574	2	Q9GRK6	Q9grk6 leishmania
121	7	3.2	377	1	CYCI_MOUSE	Q922v9 mus musculu	194	7	3.2	578	2	Q998M0	Q998m0 clostridium
122	7	3.2	377	2	Q6FH0	Q6fhh0 homo sapien	195	7	3.2	584	2	Q9V825	Q9v825 drosophila
123	7	3.2	377	2	Q8C7E2	Q8c7e2 mus musculu	196	7	3.2	584	2	Q8RXP2	Q8rxp2 arabidopsis
124	7	3.2	377	2	Q99LF2	Q99lf2 mus musculu	197	7	3.2	585	2	Q8HIF3	Q8hif3 arabidopsis
125	7	3.2	381	2	Q8RML4	Q8rml4 enterobacte	198	7	3.2	587	1	CO8B_ONCMY	Q90x85 oncorhynch
126	7	3.2	382	2	Q9KLP1	Q9klp1 vibrio chol	199	7	3.2	588	2	Q8IHE8	Q8ihe8 drosophila
127	7	3.2	385	2	Q89F02	Q89f02 bradyrhizob	200	7	3.2	596	2	Q7SXS7	Q7sxs7 brachydanio
128	7	3.2	386	2	Q6XOM9	Q6xom9 gallus gall	201	7	3.2	597	2	Q8NC94	Q8nc94 homo sapien
129	7	3.2	389	2	Q8TN02	Q8tn02 methanosarc	202	7	3.2	599	2	Q9F0Y0	Q9f0y0 pseudomonas
130	7	3.2	391	2	Q82KV8	Q82kv8 streptomyce	203	7	3.2	602	2	Q838B1	Q838b1 enterococcu
131	7	3.2	392	1	YUXJ_BACSU	P40760 bacillus su	204	7	3.2	603	2	Q9SSB2	Q9ssb2 arabidopsis
132	7	3.2	401	2	Q8WQ40	Q8wq40 leishmania	205	7	3.2	608	2	Q8BKA3	Q8bka3 m mus muscu
133	7	3.2	404	2	Q9J897	Q9j897 spodoptera	206	7	3.2	614	2	Q8YC41	Q8yc41 bruceella me
134	7	3.2	407	2	Q876V9	Q876v9 grifola umb	207	7	3.2	615	2	Q8FW84	Q8fw84 bruceella su
135	7	3.2	408	2	Q6FSI7	Q6fsi7 candida gla	208	7	3.2	625	2	Q6BI61	Q6bi61 debaryomyce
136	7	3.2	409	2	Q73GCS	Q73gcs welbachia p	209	7	3.2	632	2	Q64ZHT	Q64zht brachydanio
137	7	3.2	410	2	Q8TU92	Q8tu92 methanosarc	210	7	3.2	642	2	Q9DHT6	Q9dht6 yaba-like d
138	7	3.2	412	2	Q68EL9	Q68el9 brachydanio	211	7	3.2	659	2	Q8UJH3	Q8ujh3 pyrococcus
139	7	3.2	416	2	Q65JZ6	Q65jz6 bacillus li	212	7	3.2	663	1	GLI3_CHICK	P55879 gallus gall
140	7	3.2	417	2	Q6NTW1	Q6ntw1 xenopus lae	213	7	3.2	664	2	Q8RV6	Q8rbv6 thermoanaer
141	7	3.2	419	2	Q80UF6	Q80uf6 mus musculu	214	7	3.2	670	2	Q89EX0	Q89ex0 clostridium
142	7	3.2	420	2	Q9PUM7	Q9pum7 xenopus lae	215	7	3.2	683	2	Q6BYR0	Q6byr0 debaryomyce
143	7	3.2	421	2	Q80696	Q80696 arabidopsis	216	7	3.2	689	2	Q95Y73	Q95y73 caenorhabdi
144	7	3.2	425	2	Q7UXZ5	Q7uxz5 rhodopirell	217	7	3.2	701	2	P91922	P91922 calliphora
145	7	3.2	425	2	Q8VDP1	Q8vdp1 mus musculu	218	7	3.2	727	2	Q86KB4	Q86kb4 dictyosteli
146	7	3.2	427	2	Q80Y55	Q80y55 mus musculu	219	7	3.2	732	2	Q7RXT7	Q7rxt7 neurospora
147	7	3.2	427	2	Q8BI04	Q8bi04 mus musculu	220	7	3.2	767	2	Q90WS0	Q90ws0 fugu rubrip
148	7	3.2	430	2	Q6IAA3	Q6iaa3 homo sapien	221	7	3.2	770	2	Q8YMK4	Q8ymk4 anabaena sp
149	7	3.2	430	2	Q9NW68	Q9nw68 homo sapien	222	7	3.2	777	2	Q6CP10	Q6cp10 kluyveromyce
150	7	3.2	431	2	Q72WD7	Q72wd7 desulfovibr	223	7	3.2	779	2	Q9UI21	Q9ui21 leishmania
151	7	3.2	433	2	Q8GU14	Q8gu14 arabidopsis	224	7	3.2	791	2	Q8CUG5	Q8cug5 oceanobacil
152	7	3.2	437	2	Q6AML4	Q6aml4 desulfotale	225	7	3.2	812	2	Q9PSZ4	Q9psz4 gallus gall
153	7	3.2	438	2	Q7PYK2	Q7pyk2 anopheles g	226	7	3.2	827	2	Q6H8R9	Q6h8r9 ustilago ma
154	7	3.2	440	2	Q94A02	Q94a02 arabidopsis	227	7	3.2	828	2	Q6Z469	Q6z469 oryza sativ
155	7	3.2	441	1	YK17_SCHPO	Q94y3 schizosacch	228	7	3.2	863	1	GLND_HABIN	P43919 haemophilus
156	7	3.2	444	2	Q6CG06	Q6cg06 yarrowia li	229	7	3.2	864	1	GLND_PASMU	Q9cnh1 pasteurella
157	7	3.2	444	2	Q8YZS1	Q8yzs1 anabaena sp	230	7	3.2	868	2	Q6D3J0	Q6d3j0 erwinia car
158	7	3.2	449	2	Q8LHW3	Q8lhw3 plasmodium	231	7	3.2	885	2	Q6FKB4	Q6fkb4 candida gla
159	7	3.2	452	2	Q7R2X5	Q7r2x5 giardia lam	232	7	3.2	889	2	Q8XMY3	Q8xmy3 clostridium
160	7	3.2	454	2	Q64IX1	Q64ix1 fundulus he	233	7	3.2	904	1	MLK2_HUMAN	Q8lyj3 homo sapien
161	7	3.2	455	2	Q8G7L2	Q8g7l2 bifidobacte	234	7	3.2	920	1	AD19_MOUSE	Q35674 mus musculu
162	7	3.2	457	2	Q6LHY2	Q6lhy2 photobacter	235	7	3.2	932	2	P89499	P89499 saccharomyc
163	7	3.2	460	2	Q9H8M0	Q9h8m0 homo sapien	236	7	3.2	939	2	Q64XK8	Q64xk8 bacteroides
164	7	3.2	461	2	Q8GQ90	Q8gq90 pseudomonas	237	7	3.2	943	2	Q8BE66	Q8bee6 shewanella
165	7	3.2	465	2	Q93Q44	Q93q44 clostridium	238	7	3.2	946	1	YBT5_YEAST	P38250 saccharomyc
166	7	3.2	466	1	ATPB_CLOAB	Q92687 clostridium	239	7	3.2	947	1	MUSK_CHICK	Q8axv6 gallus gall
167	7	3.2	467	2	Q8XHZ3	Q8xhz3 clostridium	240	7	3.2	962	2	Q8PCK3	Q8pcmk3 ashpya goss
168	7	3.2	467	2	Q6NFQ8	Q6nfq8 corynebacte	241	7	3.2	962	2	Q8PUM6	Q8pum6 methanosarc
169	7	3.2	470	2	Q7NF68	Q7nf68 gloebacter	242	7	3.2	963	2	Q80VY5	Q80vy5 mus musculu
170	7	3.2	471	2	Q8GVN3	Q8gvn3 oryza sativ	243	7	3.2	964	2	Q9VNM2	Q9vnm2 lymantria d
171	7	3.2	473	2	Q65N12	Q65n12 bacillus li	244	7	3.2	985	2	Q6ES98	Q6es98 oryza sativ
172	7	3.2	474	2	Q6MZK1	Q6mzk1 homo sapien	245	7	3.2	998	1	S231_MOUSE	Q6nzc7 mus musculu
173	7	3.2	475	2	Q8GVN0	Q8gvn0 oryza sativ	246	7	3.2	1000	1	S231_HUMAN	Q9gyr8 homo sapien
174	7	3.2	476	2	Q978K1	Q978k1 thermoplasm	247	7	3.2	1014	2	Q9SHF3	Q9shf3 arabidopsis
175	7	3.2	479	2	Q7NVG3	Q7nvq3 chromobacte	248	7	3.2	1084	2	Q86IA6	Q86ia6 dictyosteli
176	7	3.2	480	2	Q90220	Q90220 agkistrodon	249	7	3.2	1123	2	Q6ZL37	Q6z137 oryza sativ
177	7	3.2	482	2	Q6BSZ9	Q6bsz9 debaryomyce	250	7	3.2	1144	2	Q6M9R8	Q6m9r8 parachlamyid

251	7	3.2	1145	2	QC7Y9	Q6c7y9	yarrowia li
252	7	3.2	1247	2	QCCLX0	Q6clx0	kluyveromyc
253	7	3.2	1257	1	PCCN RAT	P5067	rattus norv
254	7	3.2	1258	1	GLI2 HUMAN	P10070	homo sapien
255	7	3.2	1266	2	ORGU0	Q8u80	oryza sativ
256	7	3.2	1268	1	PCCN MOUSE	P5066	mus musculus
257	7	3.2	1268	2	Q6P1E3	Q6pie3	mus musculus
258	7	3.2	1274	2	Q9S2B7	Q9sz87	arabidopsis
259	7	3.2	1281	2	Q8TSN6	Q8tsn6	methanosarc
260	7	3.2	1284	2	Q23974	Q23974	drosophila
261	7	3.2	1284	2	Q3V899	Q3v899	drosophila
262	7	3.2	1296	2	QYR74	Qyr74	macaca mula
263	7	3.2	1321	1	PCCN HUMAN	O14594	homo sapien
264	7	3.2	1326	2	Q9VZF4	Q9vzf4	drosophila
265	7	3.2	1354	2	Q9W6B2	Q9w6b2	xenopus lae
266	7	3.2	1356	2	Q9NEB8	Q9neb8	leishmania
267	7	3.2	1359	2	Q752W3	Q752w3	ashbya goss
268	7	3.2	1361	2	Q9NGV2	Q9ngv2	drosophila
269	7	3.2	1361	2	Q9V714	Q9v714	drosophila
270	7	3.2	1609	1	FIG2 YEAST	P25653	saccharomyc
271	7	3.2	1683	1	LM07 HUMAN	Q8w11	homo sapien
272	7	3.2	1721	2	Q835A4	Q835a4	enterococcu
273	7	3.2	1734	2	Q8MKW9	Q8mkw9	drosophila
274	7	3.2	1743	2	Q966V0	Q966v0	drosophila
275	7	3.2	1842	2	Q6CUT9	Q6cut9	kluyveromyc
276	7	3.2	2205	2	Q7KRf5	Q7krf5	drosophila
277	7	3.2	2237	2	Q7RQ19	Q7rq19	plasmodium
278	7	3.2	2515	2	Q24551	Q24551	drosophila
279	7	3.2	2555	2	Q8T9E3	Q8t9e3	drosophila
280	7	3.2	2559	2	Q44113	Q44113	drosophila
281	7	3.2	2559	2	Q44381	Q44381	drosophila
282	7	3.2	2559	2	Q9V7X3	Q9v7x3	drosophila
283	7	3.2	2633	2	Q7OK12	Q7ok12	anopheles g
284	7	3.2	2669	2	Q9MY8	Q9my8	mus musculus
285	7	3.2	2671	2	Q754A3	Q754a3	ashbya goss
286	7	3.2	2731	2	O18366	O18366	drosophila
287	7	3.2	2731	2	O61307	O61307	drosophila
288	7	3.2	2731	2	Q9VNU6	Q9vnu6	drosophila
289	7	3.2	2870	2	Q97LF2	Q97lf2	clostridium
290	7	3.2	2969	2	Q5NR48	Q5nr48	homo sapien
291	7	3.2	2974	2	Q815L7	Q815l7	plasmodium
292	7	3.2	3153	2	Q6C6F9	Q6c6f9	yarrowia li
293	7	3.2	3469	2	Q9U412	Q9u412	drosophila
294	7	3.2	3604	2	Q9VYK0	Q9vyk0	drosophila
295	7	3.2	3657	2	Q96Q15	Q96q15	homo sapien
296	7	3.2	3684	1	UPL1 ARATH	Q8gy23	arabidopsis
297	7	3.2	4753	2	Q8PLJ3	Q8plj3	xanthomonas
298	7	3.2	6315	2	Q9ADL6	Q9adl6	polyangium
299	7	3.2	6973	2	Q7QXR7	Q7qxr7	giardia lam
300	6	2.8	25	2	Q6QH14	Q6ghi4	leptosphaer
301	6	2.8	27	2	Q91JP4	Q91jf4	hepatitis c
302	6	2.8	32	2	Q44509	Q44509	azotobacter
303	6	2.8	33	2	Q7M1R4	Q7m1r4	spinacia ol
304	6	2.8	38	2	Q7P8V1	Q7p8v1	rickettsia
305	6	2.8	41	2	Q739F1	Q739f1	bacillus ce
306	6	2.8	46	2	Q87NG9	Q87ng9	vibrio para
307	6	2.8	47	2	Q23578	Q23578	caenorhabdi
308	6	2.8	48	2	Q9AIN3	Q9ain3	streptococc
309	6	2.8	48	2	Q879N9	Q879n9	streptococc
310	6	2.8	48	2	Q9Q577	Q9q577	human immun
311	6	2.8	49	2	Q811J1	Q811j1	drosophila
312	6	2.8	49	2	Q9Q578	Q9q578	human immun
313	6	2.8	49	2	Q9Q580	Q9q580	human immun
314	6	2.8	50	2	Q9PG59	Q9pg59	xytella fas
315	6	2.8	50	2	Q65342	Q65342	autographa
316	6	2.8	55	2	Q96X16	Q96xl6	sulfolobus
317	6	2.8	55	2	Q67KQ3	Q67kq3	symbiobacte
318	6	2.8	55	2	Q83EJ5	Q83ej5	coxiella bu
319	6	2.8	56	2	Q9K9E1	Q9k9e1	bacillus ha
320	6	2.8	58	2	Q44EL5	Q44el5	uncultured
321	6	2.8	59	2	Q41936	Q41936	arabidopsis
322	6	2.8	59	2	Q81R19	Q81r19	bacillus an
323	6	2.8	61	2	Q6K483	Q6k483	oryza sativ

324	6	2.8	61	2	Q99M06	Q99mq6	cricketulus
325	6	2.8	63	1	SIFA MAIZE	P42554	zea mays (m
326	6	2.8	64	2	Q91Y98	Q91y98	mus musculu
327	6	2.8	65	2	O6LTF6	Q6ltf6	photobacter
328	6	2.8	65	2	Q91Q25	Q91q25	carcopithec
329	6	2.8	68	2	Q7Q2F5	Q7q2f5	giardia lam
330	6	2.8	69	1	COF2_ENTHR	Q47840	enterococcu
331	6	2.8	70	2	Q7Z4B4	Q7z4b4	homo sapien
332	6	2.8	70	2	O6H2R5	Q6hzr5	bacillus an
333	6	2.8	70	2	Q63CB1	Q63cb1	bacillus ce
334	6	2.8	70	2	Q7W9G7	Q7w9g7	bordetella
335	6	2.8	70	2	Q7WH95	Q7wh95	bordetella
336	6	2.8	70	2	Q9CKF1	Q9ckp1	pasteurella
337	6	2.8	70	2	O6HJ53	Q6hjs3	bacillus th
338	6	2.8	71	2	Q63UR7	Q63ur7	burkholderi
339	6	2.8	71	2	Q7NSV8	Q7nsv8	chromobacte
340	6	2.8	71	2	Q9PI59	Q9pi59	campylobact
341	6	2.8	72	2	Q7PRD3	Q7prd3	anopheles g
342	6	2.8	72	2	Q81EE1	Q81eel	bacillus ce
343	6	2.8	72	2	Q86918	Q86918	human t-lym
344	6	2.8	73	2	Q7PQH8	Q7pqh8	anopheles g
345	6	2.8	73	2	Q7PU29	Q7pu29	anopheles g
346	6	2.8	73	2	Q62586	Q62586	peromyscus
347	6	2.8	73	2	Q64372	Q64372	peromyscus
348	6	2.8	74	2	Q9LLN8	Q9lln8	oryza sativ
349	6	2.8	74	2	Q7MSL5	Q7msl5	wolinella s
350	6	2.8	74	2	Q7WBF5	Q7wbf5	bordetella
351	6	2.8	74	2	Q7WMX6	Q7wmx6	bordetella
352	6	2.8	75	2	Q6AX78	Q6ax78	xenopus lae
353	6	2.8	79	2	Q7PE02	Q7pe02	anopheles g
354	6	2.8	79	2	Q7PEF7	Q7pef7	anopheles g
355	6	2.8	79	2	Q7PIW0	Q7piw0	anopheles g
356	6	2.8	82	2	Q7YX33	Q7yx33	caenorhabdi
357	6	2.8	82	2	O22634	O22634	oryza sativ
358	6	2.8	82	2	Q6K3Y6	Q6k3y6	oryza sativ
359	6	2.8	85	2	Q64660	Q64660	cavia (guin
360	6	2.8	85	2	Q80844	Q80844	hantavirus
361	6	2.8	88	2	Q8RZG8	Q8rzg8	oryza sativ
362	6	2.8	89	1	PERC_ECO27	P43475	escherichia
363	6	2.8	89	2	Q8S6T9	Q8s6t9	oryza sativ
364	6	2.8	89	2	Q7Y1K5	Q7y1k5	oryza sativ
365	6	2.8	89	2	Q9APE4	Q9ape4	escherichia
366	6	2.8	89	2	Q9EUG3	Q9eug3	escherichia
367	6	2.8	89	2	Q9F874	Q9f874	escherichia
368	6	2.8	89	2	Q9F883	Q9f883	escherichia
369	6	2.8	89	2	Q7DJS3	Q7djs3	escherichia
370	6	2.8	90	2	Q8W2H5	Q8w2h5	setaria ver
371	6	2.8	90	2	Q8W2J0	Q8w2j0	setaria fab
372	6	2.8	91	1	UTER HUMAN	P11684	homo sapien
373	6	2.8	91	2	Q6FJ46	Q6fj46	candida gla
374	6	2.8	91	2	Q9BNQ8	Q9bnq8	milnesium t
375	6	2.8	91	2	Q75LQ5	Q75lq5	oryza sativ
376	6	2.8	91	2	Q72749	Q72749	human immun
377	6	2.8	92	2	Q6ARR7	Q6arr7	desulfotale
378	6	2.8	93	2	Q6ESP6	Q6esp6	oryza sativ
379	6	2.8	93	2	Q7BV71	Q7bv71	salmonella
380	6	2.8	93	2	Q6LJ48	Q6lj48	photobacter
381	6	2.8	93	2	Q75382	Q75382	human immun
382	6	2.8	95	2	Q7KUG7	Q7kug7	drosophila
383	6	2.8	96	2	Q92EA1	Q92ea1	listeria in
384	6	2.8	96	2	Q83JN4	Q83jn4	shigella fl
385	6	2.8	97	2	Q7RDA7	Q7rda7	plasmodium
386	6	2.8	97	2	Q62JY2	Q62jy2	burkholderi
387	6	2.8	98	2	O22789	O22789	arabidopsis
388	6	2.8	98	2	Q82R21	Q82r21	streptomyce
389	6	2.8	99	2	Q7DDB1	Q7ddb1	neisseria m
390	6	2.8	99	2	Q9J9R3	Q9jr93	neisseria m
391	6	2.8	100	2	O58249	O58249	pyrococcus
392	6	2.8	100	2	Q8GVH1	Q8gvh1	oryza sativ
393	6	2.8	100	2	Q6GM33	Q6gm33	xenopus lae
394	6	2.8	101	2	Q14476	Q14476	homo sapien
395	6	2.8	101	2	Q9VDS4	Q9vds4	drosophila
396	6	2.8	101	2	O86332	O86332	mycobacteri

397	6	2.8	101	2	Q7U194	Q7u194 mycobacteri	470	6	2.8	116	2	Q6XFX2	O6xfx2 nectarinia
398	6	2.8	101	2	Q9C723	Q9ctz3 mus musculus	471	6	2.8	116	2	Q6XFX5	O6xfx5 nectarinia
399	6	2.8	101	2	Q8QVL7	Q8qvl7 tt virus. o	472	6	2.8	116	2	Q6XFX9	O6xfx9 nectarinia
400	6	2.8	102	1	YAC1_MAIZE	P08771 zea mays (m	473	6	2.8	116	2	Q6XFY0	O6xfy0 nectarinia
401	6	2.8	102	2	Q8KG24	Q8kg24 chlorobium	474	6	2.8	116	2	Q6XFY1	O6xfy1 anthrepes
402	6	2.8	102	2	Q64098	Q64098 mus sp. tru	475	6	2.8	116	2	Q8GI75	O8gi75 salmonella
403	6	2.8	103	2	Q9YAP0	Q9yap0 aeropyrum p	476	6	2.8	116	2	Q8V2N5	O8v2n5 camelpox vi
404	6	2.8	103	2	Q6GMW9	Q6gmw9 homo sapien	477	6	2.8	116	2	Q6ZV15	O6zv15 pyrobaculum
405	6	2.8	104	1	FSP8_ECOLI	P23857 escherichia	478	6	2.8	116	2	Q775Q6	O775q6 camelpox vi
406	6	2.8	104	2	Q42216	Q42216 arabidopsis	479	6	2.8	116	2	Q9JF81	Q9jfb1 vaccinia vi
407	6	2.8	104	2	Q8CW40	Q8cw40 escherichia	480	6	2.8	117	1	VA21_VACCC	P33844 variola vir
408	6	2.8	104	2	Q8D8D5	Q8d8d5 vibrio vuln	481	6	2.8	117	1	VA21_VARV	Q975f3 sulfolobus
409	6	2.8	105	2	Q82823	Q82823 pseudomonas	482	6	2.8	117	2	Q975F3	O871k4 neurospora
410	6	2.8	105	2	Q8G115	Q8gi15 pseudomonas	483	6	2.8	117	2	Q871K4	O9gku0 macaca fasc
411	6	2.8	105	2	Q739J5	Q739j5 bacillus ce	484	6	2.8	117	2	Q9GKU0	O9gcb5 mycobacteri
412	6	2.8	105	2	Q924A3	Q924a3 mus musculus	485	6	2.8	117	2	Q9CBX5	O8gmt3 cowpox viru
413	6	2.8	105	2	Q8C5P4	Q8c5p4 mus musculus	486	6	2.8	117	2	Q8QMT3	O6rzg2 rabbitpox v
414	6	2.8	106	2	Q70M31	Q70m31 natronomona	487	6	2.8	117	2	Q6RZG2	O76py0 variola min
415	6	2.8	106	2	Q70M33	Q70m33 halorubrum	488	6	2.8	117	2	Q76PY0	O76q16 cowpox viru
416	6	2.8	106	2	Q84N88	Q84n88 cadia purpu	489	6	2.8	117	2	Q76Q16	O76p88 vaccinia vi
417	6	2.8	107	2	Q8WY21	Q8wy21 homo sapien	490	6	2.8	117	2	Q76ZP8	O77266 sulfolobus
418	6	2.8	108	2	Q7RT15	Q7rt15 plasmodium	491	6	2.8	118	2	Q97Z66	Q21028 caenorhabdi
419	6	2.8	109	2	Q7PHS4	Q7phs4 anopheles g	492	6	2.8	118	2	Q21028	O6ypx1 onion yello
420	6	2.8	109	2	Q7Q7U1	Q7q7u1 anopheles g	493	6	2.8	118	2	Q6YPX1	O8j194 ectromelia
421	6	2.8	109	2	Q9PB20	Q9pb20 campylobact	494	6	2.8	118	2	Q8JL94	O6ili0 drosophila
422	6	2.8	110	2	Q855P1	Q855p1 mycobacteri	495	6	2.8	119	2	Q6ILL0	O8pwb8 methanosarc
423	6	2.8	110	2	Q8DLH7	Q8dlh7 synechococc	496	6	2.8	120	2	Q8PVB8	O6ytr4 oryza sativ
424	6	2.8	111	2	Q6ZNM0	Q6znm0 homo sapien	497	6	2.8	120	2	Q6YTR4	O82xb7 nitrosomona
425	6	2.8	111	2	Q6DY61	Q6dy61 nectarinia	498	6	2.8	120	2	Q82XB7	O93xr8 bruguiera g
426	6	2.8	111	2	Q6DY62	Q6dy62 nectarinia	499	6	2.8	121	2	Q93XR8	O67uu3 oryza sativ
427	6	2.8	111	2	Q6DY64	Q6dy64 nectarinia	500	6	2.8	121	2	Q67UU3	O84n74 machaerium
428	6	2.8	111	2	Q6DY65	Q6dy65 nectarinia	501	6	2.8	121	2	Q84N74	Q7vip5 prochloroco
429	6	2.8	111	2	Q6DY66	Q6dy66 nectarinia	502	6	2.8	121	2	Q7V1P5	O8flm2 corynebacte
430	6	2.8	111	2	Q6DY98	Q6dy98 nectarinia	503	6	2.8	121	2	Q8FLM2	O6mcz2 parachlamyd
431	6	2.8	111	2	Q6DYA1	Q6dya1 nectarinia	504	6	2.8	121	2	Q6MCZ2	O66897 four corner
432	6	2.8	111	2	Q6DYA2	Q6dya2 nectarinia	505	6	2.8	121	2	Q66897	O6zh83 oryza sativ
433	6	2.8	111	2	Q6DYA5	Q6dya5 nectarinia	506	6	2.8	122	2	Q6ZHG3	O6lsg5 photobacter
434	6	2.8	111	2	Q76Z05	Q76z05 bacterioph	507	6	2.8	122	2	Q6LSG5	O14474 homo sapien
435	6	2.8	112	2	Q8GU28	Q8gu28 polytomella	508	6	2.8	123	2	Q8FG00	O8fg00 escherichia
436	6	2.8	113	2	Q64C64	Q64c64 uncultured	509	6	2.8	123	2	Q14474	O8x710 escherichia
437	6	2.8	113	2	Q57817	O57817 pyrococcus	510	6	2.8	123	2	Q83KI3	O83kl3 shigella fl
438	6	2.8	113	2	Q8TNN3	Q8tnn3 methanosarc	511	6	2.8	124	2	Q7V597	O7v597 bacterioph
439	6	2.8	113	2	Q8ZZP8	Q8zzp8 pyrobaculum	512	6	2.8	124	2	Q8TS70	O8ts70 methanosarc
440	6	2.8	113	2	Q86XP5	Q86xp5 homo sapien	513	6	2.8	126	2	Q6ZT32	O6zt32 homo sapien
441	6	2.8	113	2	Q7PEP9	Q7pep9 anopheles g	514	6	2.8	126	2	Q6ZT32	O8ct85 staphylococ
442	6	2.8	113	2	Q6AAJ9	Q6aaj9 propionibac	515	6	2.8	126	2	Q8CT85	O8cs17 mus musculus
443	6	2.8	113	2	Q8DAJ3	Q8daj3 vibrio vuln	516	6	2.8	126	2	Q8CS17	O73616 xenopus lae
444	6	2.8	114	1	YHT8_YEAST	P38841 saccharomyc	517	6	2.8	127	2	Q73616	O856g8 mycobacteri
445	6	2.8	114	2	Q6XFG9	Q6xfg9 nectarinia	518	6	2.8	128	2	Q8N7N0	O8n7n0 homo sapien
446	6	2.8	114	2	Q6ETH8	Q6eth8 oryza sativ	519	6	2.8	128	2	Q9EVJ5	O9evj5 edta-degrad
447	6	2.8	114	2	Q81PU2	Q81p2 bacillus an	520	6	2.8	128	2	Q9EVJ5	O9unl6 homo sapien
448	6	2.8	115	2	Q6XFF0	Q6xff0 nectarinia	521	6	2.8	129	2	Q9UNL6	O7qx87 giardia lam
449	6	2.8	115	2	Q6XFF2	Q6xff2 nectarinia	522	6	2.8	129	2	Q7QX87	O9izl0 simian t-ly
450	6	2.8	115	2	Q6HHT1	Q6hht1 bacillus th	523	6	2.8	129	2	Q9IZL0	O9ycb5 aeropyrum p
451	6	2.8	115	2	Q83RL0	Q83rl0 shigella fl	524	6	2.8	130	2	Q9YCB5	O70a15 triticum ae
452	6	2.8	115	2	Q8V4V7	Q8v4v7 monkeypox v	525	6	2.8	131	2	Q70A15	O70a15 triticum ae
453	6	2.8	116	2	Q6JGMO	Q6jgm0 todistrostru	526	6	2.8	131	2	Q83B98	O83b98 coxiella bu
454	6	2.8	116	2	Q6XFF4	Q6xff4 nectarinia	527	6	2.8	132	1	RR12_CHLRE	P14149 chlamydomon
455	6	2.8	116	2	Q6XFF5	Q6xff5 nectarinia	528	6	2.8	132	2	Q70JC2	O70jc2 bacillus li
456	6	2.8	116	2	Q6XFF6	Q6xff6 nectarinia	529	6	2.8	132	2	Q98B24	O98b24 rhizobium l
457	6	2.8	116	2	Q6XFF7	Q6xff7 nectarinia	530	6	2.8	133	2	Q8UOR1	O8uor1 pyrococcus
458	6	2.8	116	2	Q6XFF9	Q6xff9 nectarinia	531	6	2.8	133	2	Q21887	Q21887 caenorhabdi
459	6	2.8	116	2	Q6XFFA	Q6xffa nectarinia	532	6	2.8	133	2	Q6H4G7	O6h4g7 oryza sativ
460	6	2.8	116	2	Q6XFF5	Q6xff5 nectarinia	533	6	2.8	133	2	Q92GJ7	O92gj7 rickettsia
461	6	2.8	116	2	Q6XFF6	Q6xff6 nectarinia	534	6	2.8	133	2	Q9CRX9	O9crx9 mus musculu
462	6	2.8	116	2	Q6XFF8	Q6xff8 nectarinia	535	6	2.8	134	2	Q8T352	O8t352 plasmodium
463	6	2.8	116	2	Q6XFG1	Q6xfg1 nectarinia	536	6	2.8	134	2	Q25078	O25078 helicobacte
464	6	2.8	116	2	Q6XFG4	Q6xfg4 nectarinia	537	6	2.8	134	2	Q9ZMC8	O9zmc8 mus musculu
465	6	2.8	116	2	Q6XFG7	Q6xfg7 nectarinia	538	6	2.8	134	2	Q9ZMC8	O9zmc8 mus musculu
466	6	2.8	116	2	Q6XFG8	Q6xfg8 nectarinia	539	6	2.8	136	2	Q9CRZ2	O62434 caenorhabdi
467	6	2.8	116	2	Q6XFH0	Q6xfh0 nectarinia	540	6	2.8	136	2	O62434	O7r6a8 giardia lam
468	6	2.8	116	2	Q6XPH3	Q6xph3 nectarinia	541	6	2.8	136	2	Q7R6A8	O7r6a8 giardia lam
469	6	2.8	116	2	Q6XPH5	Q6xph5 nectarinia	542	6	2.8	137	2	Q9WNX1	O9wnx1 human t-lym
			116	2	Q6XFX0	O6xfx0 nectarinia		6	2.8				Q70M34 halobacteri

543	6	2.8	138	2	Q6BN70	Q6bn70 debaryomyce	616	6	2.8	146	1	HBG_MACNE	P02097 macaca neme
544	6	2.8	139	2	Q6ZUI3	Q6zui3 homo sapien	617	6	2.8	146	1	HBG_PAPCY	P68079 papio cynoc
545	6	2.8	139	2	Q6GRS1	Q6grs1 hammodium	618	6	2.8	146	1	HBG_TARBA	P68079 tarsius ban
546	6	2.8	139	2	Q7NFX2	Q7nfx2 gloeobacter	619	6	2.8	146	1	P8TFA_BACSU	P26379 bacillus su
547	6	2.8	140	2	Q59311	Q59311 pyrococcus	620	6	2.8	146	1	Q8GT54	P8gt54 hordeum vul
548	6	2.8	140	2	Q6ZR24	Q6zr24 homo sapien	621	6	2.8	146	2	Q6TIM6	Q6tim6 staphylococ
549	6	2.8	140	2	Q6ZVP1	Q6zvp1 homo sapien	622	6	2.8	146	2	Q6TIM7	Q6tim7 staphylococ
550	6	2.8	140	2	Q8LA12	Q8la12 arabidopsis	623	6	2.8	146	2	Q6TIM1	Q6tim1 staphylococ
551	6	2.8	140	2	Q93NE0	Q93ne0 myxococcus	624	6	2.8	146	2	Q6TIM3	Q6tim3 staphylococ
552	6	2.8	140	2	Q87IX2	Q87ix2 vibrio para	625	6	2.8	146	2	Q6TIM4	Q6tim4 staphylococ
553	6	2.8	141	2	Q6IKR8	Q6ikr8 drosophila	626	6	2.8	146	2	Q6TIM1	Q6tim1 staphylococ
554	6	2.8	141	2	Q8GX01	Q8gx01 arabidopsis	627	6	2.8	146	2	Q84G94	Q84g94 staphylococ
555	6	2.8	141	2	Q9C7Q8	Q9c7q8 arabidopsis	628	6	2.8	146	2	Q84G95	Q84g95 staphylococ
556	6	2.8	141	2	Q9CRT1	Q9crt1 mus musculus	629	6	2.8	146	2	Q84G96	Q84g96 staphylococ
557	6	2.8	141	2	Q84663	Q84663 paramacium	630	6	2.8	146	2	Q8F267	Q8f267 leptospira
558	6	2.8	142	1	RL11_BRUME	RL11brume brucella me	631	6	2.8	146	2	Q9QUN8	Q9qun8 mus musculus
559	6	2.8	142	1	RL11_BRUSU	RL11brusu brucella su	632	6	2.8	146	2	Q9QUT6	Q9qut6 rattus sp.
560	6	2.8	142	1	Q95233	Q95233 perodicticu	633	6	2.8	146	2	Q9QW91	Q9qw91 rattus sp.
561	6	2.8	142	2	Q6TIN8	Q6tin8 staphylococ	634	6	2.8	146	2	Q9R0S6	Q9r0s6 mus musculus
562	6	2.8	142	2	Q9YMS0	Q9yms0 lymantria d	635	6	2.8	146	2	Q7TIF0	Q7tif0 geochelone
563	6	2.8	142	2	Q29967	Q29967 archaeoglob	636	6	2.8	147	1	HBG_TARSY	P18436 tarsius syr
564	6	2.8	143	2	Q48527	Q48527 lactobacill	637	6	2.8	147	1	Q96FH6	Q96fh6 homo sapien
565	6	2.8	143	2	Q82G13	Q82g13 streptomyce	638	6	2.8	147	2	Q96FH7	Q96fh7 homo sapien
566	6	2.8	143	2	Q8D6B9	Q8d6b9 vibrio vuln	639	6	2.8	147	2	Q68NH9	Q68nh9 homo sapien
567	6	2.8	143	2	Q8DAJ2	Q8daj2 vibrio vuln	640	6	2.8	147	2	Q03903	Q03903 macaca mula
568	6	2.8	144	2	Q72K31	Q72k31 thermus the	641	6	2.8	147	2	Q9F562	Q9f562 escherichia
569	6	2.8	145	2	P74671	P74671 synechocyst	642	6	2.8	147	2	Q88752	Q88752 rattus norv
570	6	2.8	145	2	Q6FLX6	Q6flx6 mesoplasma	643	6	2.8	147	2	Q91V86	Q91v86 m mus muscu
571	6	2.8	146	1	HBB1_MOUSE	P02088 mus musculus	644	6	2.8	147	2	Q9CR49	Q9cr49 m mus muscu
572	6	2.8	146	1	HBB1_RAT	P02091 rattus norv	645	6	2.8	147	2	Q9CXH5	Q9cxh5 mus musculus
573	6	2.8	146	1	HBB2_MOUSE	P02089 mus musculus	646	6	2.8	147	2	Q9CY12	Q9cy12 mus musculus
574	6	2.8	146	1	HBB2_RAT	P11517 rattus norv	647	6	2.8	147	2	Q9CY54	Q9cy54 mus musculus
575	6	2.8	146	1	HBB_CAVPO	P02095 cavia porce	648	6	2.8	147	2	Q9D0B2	Q9d0b2 mus musculus
576	6	2.8	146	1	HBB_CYNBP	P11754 cynopterus	649	6	2.8	147	2	Q95W24	Q95w24 anthonomus
577	6	2.8	146	1	HBB_GEONI	P83123 geochelone	650	6	2.8	148	2	Q65T42	Q65t42 bacillus li
578	6	2.8	146	1	HBB_MARMA	P08853 marmota mar	651	6	2.8	149	2	Q9GMG9	Q9gm9 macaca mula
579	6	2.8	146	1	HBB_MESAU	P02094 mesocricetu	652	6	2.8	149	2	Q6W3M8	Q6w3m8 alvinella p
580	6	2.8	146	1	HBB_MESBR	P18707 mesocricetu	653	6	2.8	149	2	Q7NIN2	Q7nin2 photorhabdu
581	6	2.8	146	1	HBB_MICXA	P02092 microtus xa	654	6	2.8	149	2	Q9WNX0	Q9wnx0 human t-lym
582	6	2.8	146	1	HBB_PSIKR	P21668 psittacula	655	6	2.8	150	1	TRPE_CITFR	P00896 citrobacter
583	6	2.8	146	1	HBB_PTEAL	P14391 pteropus al	656	6	2.8	150	2	Q6MAN8	Q6man8 parachlamyd
584	6	2.8	146	1	HBB_ROUAE	P02058 roussettu a	657	6	2.8	151	2	Q75ZP4	Q75zp4 haemadipsa
585	6	2.8	146	1	HBB_SPECI	P09421 spermophilu	658	6	2.8	151	2	Q7Y4Z1	Q7y4z1 bacterioph
586	6	2.8	146	1	HBB_SPETO	P07410 spermophilu	659	6	2.8	151	2	Q855Z3	Q855z3 mycobacteri
587	6	2.8	146	1	HBB_SUNMU	P02060 suncus muri	660	6	2.8	151	2	Q8KJ09	Q8kj09 vibrio angu
588	6	2.8	146	1	HBB_TADBR	P11756 tadarida br	661	6	2.8	151	2	Q8R738	Q8r738 thermocanaer
589	6	2.8	146	1	HBB_TALEU	P02061 talpa europ	662	6	2.8	152	1	V57B_BP74	P04533 bacterioph
590	6	2.8	146	1	HBB_TRIIN	P07415 trichechus	663	6	2.8	152	2	Q14491	Q14491 homo sapien
591	6	2.8	146	1	HBE1_CAPHI	P02102 capra hircu	664	6	2.8	152	2	Q8B571	Q8b571 pseudocowpo
592	6	2.8	146	1	HBE_CHEME	Q28338 cheirogaleu	665	6	2.8	152	2	Q6EEB2	Q6eeb2 latimeria c
593	6	2.8	146	1	HBE_DAUWA	Q28356 daubentonia	666	6	2.8	153	1	YIBG_ECOLI	P32106 escherichia
594	6	2.8	146	1	HBE_DIDMA	P11025 didelphis m	667	6	2.8	153	2	Q7SGT4	Q7sgt4 neurospora
595	6	2.8	146	1	HBE_EULFU	P08223 eulemur ful	668	6	2.8	153	2	Q8MVN3	Q8mvn3 boltenia vi
596	6	2.8	146	1	HBE_GALCR	P19759 galago cras	669	6	2.8	153	2	Q94L78	Q94lt8 oryza sativ
597	6	2.8	146	1	HBE_MACRU	P81042 macropus eu	670	6	2.8	153	2	Q8XDH3	Q8xdh3 escherichia
598	6	2.8	146	1	HBE_MICMU	Q28496 microcebus	671	6	2.8	154	2	Q7X127	Q7x127 oryza sativ
599	6	2.8	146	1	HBE_MOUSE	P02104 mus musculus	672	6	2.8	154	2	Q9SHG7	Q9shg7 arabidopsis
600	6	2.8	146	1	HBE_SMICR	Q28931 smnithopsis	673	6	2.8	155	2	Q14403	Q14403 homo sapien
601	6	2.8	146	1	HBG1_GORGO	P62741 gorilla gor	674	6	2.8	155	2	Q80312	Q80312 bacterioph
602	6	2.8	146	1	HBG1_HYLLA	P61947 hylobates l	675	6	2.8	155	2	Q3Y3A5	Q3y3a5 bacillus ce
603	6	2.8	146	1	HBG1_PANPA	Q28779 pan paniscu	676	6	2.8	155	2	Q63EA2	Q63ee2 bacillus ce
604	6	2.8	146	1	HBG1_PANTR	P61920 pan troglod	677	6	2.8	155	2	Q8XPV4	Q8xpv4 ralstonia s
605	6	2.8	146	1	HBG1_PONPY	P18995 pongo pygma	678	6	2.8	155	2	Q6MRI9	Q6mri9 bdellovibri
606	6	2.8	146	1	HBG2_GORGO	P62742 gorilla gor	679	6	2.8	155	2	Q73BS3	Q73bs3 bacillus ce
607	6	2.8	146	1	HBG2_HYLLA	P61948 hylobates l	680	6	2.8	155	2	Q746S1	Q746s1 geobacter s
608	6	2.8	146	1	HBG2_PANTR	P61921 pan troglod	681	6	2.8	156	2	Q81GH8	Q81gh8 bacillus ce
609	6	2.8	146	1	HBG2_PONPY	P18996 pongo pygma	682	6	2.8	156	2	Q81TN3	Q81tn3 bacillus an
610	6	2.8	146	1	HBG_CHEME	P08224 cheirogaleu	683	6	2.8	156	2	Q6EEB1	Q6eeb1 prototenus
611	6	2.8	146	1	HBG_EULFU	P08225 eulemur ful	684	6	2.8	157	2	Q68SU5	Q68su5 pleurotus d
612	6	2.8	146	1	HBG_GALCR	P19760 galago cras	685	6	2.8	157	2	Q6ZUY2	Q6zuy2 homo sapien
613	6	2.8	146	1	HBG_HUMAN	P62027 homo sapien	686	6	2.8	157	2	Q8T0I3	Q8t0i3 drosophila
614	6	2.8	146	1	HBG_MACFU	P68078 macaca fusc	687	6	2.8	157	2	Q9LTK4	Q9ltk4 arabidopsis
615	6	2.8	146	1	HBG_MACMU	P68077 macaca mula	688	6	2.8	157	2	Q6HLV9	Q6hlv9 bacillus th

689	2.8	6	157	2	Q7ZZT8	Q7zzt8 oreochromis	762	6	2.8	176	2	Q8DHY0	Q8dhy0 synechococ
690	2.8	6	158	1	Y052_ARCFU	O30184 archaeoglob	763	6	2.8	176	2	Q8E8G6	Q8e8g6 shewanella
691	2.8	6	158	2	Q7SD90	Q7sd90 neurospora	764	6	2.8	177	2	Q7IS60	Q7is60 homo sapien
692	2.8	6	158	2	Q69ML0	Q69ml0 oryza sativ	765	6	2.8	177	2	Q9FQQ9	Q9fgq9 arabidopsis
693	2.8	6	158	2	Q9XC44	Q9xc44 methylococ	766	6	2.8	177	2	Q63HA4	Q63ha4 bacillus ce
694	2.8	6	158	2	Q7TWI3	Q7twi3 mycobacteri	767	6	2.8	177	2	Q73PB0	Q73pb0 bacillus ce
695	2.8	6	158	2	Q9KSB7	Q9ksb7 vibrio chol	768	6	2.8	177	2	Q81J54	Q81j54 bacillus ce
696	2.8	6	158	2	Q6PA17	Q6pa17 xenopus lae	769	6	2.8	177	2	Q81VU4	Q81vu4 bacillus an
697	2.8	6	159	2	Q9VA42	Q9va42 drosophila	770	6	2.8	177	2	Q6HPS2	Q6hps2 bacillus th
698	2.8	6	159	2	Q6TFX5	Q6tfx5 erwinia amy	771	6	2.8	177	2	Q6KYJ3	Q6kyj3 bacillus an
699	2.8	6	159	2	Q706U6	Q706u6 pseudomonas	772	6	2.8	178	1	LACB_BOVIN	P02754 bos taurus
700	2.8	6	159	2	Q8GFV4	Q8gfv4 citrobacter	773	6	2.8	178	2	Q7Q9E8	Q7q9e8 anopheles g
701	2.8	6	159	2	Q9EWQ9	Q9ewq9 streptomyce	774	6	2.8	178	2	Q84363	Q84363 chlamydia t
702	2.8	6	159	2	Q8BL68	Q8bl68 mus musculu	775	6	2.8	178	2	Q8EWG5	Q8ewg5 mycoplasma
703	2.8	6	159	2	Q75XW6	Q75xw6 fugu rubrip	776	6	2.8	179	1	FRIH_CHICK	P08267 gallus gall
704	2.8	6	160	1	ISPP_THETN	Q8r7s8 thermoanaer	777	6	2.8	179	2	Q6IGW9	Q6igw9 drosophila
705	2.8	6	160	2	Q7QAI0	Q7qai0 anopheles g	778	6	2.8	179	2	Q84KF3	Q84kf3 glycine max
706	2.8	6	160	2	Q46174	Q46174 clostridium	779	6	2.8	179	2	Q84IF3	Q84if3 selenomonas
707	2.8	6	160	2	Q89BK0	Q89bk0 bradyrhizob	780	6	2.8	179	2	Q8RGJ3	Q8rgj3 fusbacteri
708	2.8	6	162	1	IL2_CEREL	P51747 cervus elap	781	6	2.8	180	1	FRIH_PIG	P19130 sus scrofa
709	2.8	6	162	1	LACB_OVIMU	P67975 ovis orient	782	6	2.8	180	1	LACB_BUBBU	P02755 bubalus bub
710	2.8	6	162	2	Q9UK75	Q9uk75 homo sapien	783	6	2.8	180	1	LACB_CAPHI	P02756 capra hircu
711	2.8	6	162	2	Q9MG88	Q9mg88 chrysodidym	784	6	2.8	180	1	LACB_SHEEP	P67976 ovis aries
712	2.8	6	162	2	Q7X143	Q7x143 oryza sativ	785	6	2.8	180	2	Q9HKQ7	Q9hkq7 thermoplasm
713	2.8	6	163	2	Q6ZVB8	Q6zvb8 homo sapien	786	6	2.8	180	2	Q96Z17	Q96z17 dermatophag
714	2.8	6	163	2	Q7V890	Q7v890 prochloroco	787	6	2.8	180	2	Q6FE64	Q6fef6 acinetobact
715	2.8	6	164	1	FRIH_RABIT	P25915 oryctolagus	788	6	2.8	180	2	Q72LQ5	Q72lq5 thermus the
716	2.8	6	164	2	Q73N39	Q73n39 treponema d	789	6	2.8	181	1	APT2_YEAST	P36973 saccharomyc
717	2.8	6	165	2	Q8TD27	Q8td27 homo sapien	790	6	2.8	181	1	FRIH_MOUSE	P09528 mus musculu
718	2.8	6	165	2	Q9DFE9	Q9dfe9 oncorhynch	791	6	2.8	181	1	FRIH_RAT	P19132 rattus norv
719	2.8	6	166	1	RS5_BACAN	Q81vr3 bacillus an	792	6	2.8	181	2	Q7OK06	Q7ok06 anopheles g
720	2.8	6	166	2	Q8WZ00	Q8wx00 homo sapien	793	6	2.8	181	2	Q8RSP9	Q8rsp9 rhizobium l
721	2.8	6	166	2	Q9L2P2	Q9l2p2 arabidopsis	794	6	2.8	181	2	Q6REG9	Q6reg9 rhodococcus
722	2.8	6	166	2	Q63H73	Q63h73 bacillus ce	795	6	2.8	181	2	Q6PRV1	Q6prv1 coturnix co
723	2.8	6	166	2	Q73F79	Q73f79 bacillus ce	796	6	2.8	182	1	FRIH_HUMAN	P02794 homo sapien
724	2.8	6	166	2	Q6HPP1	Q6hpp1 bacillus th	797	6	2.8	182	1	FRIH_TRIVU	Q6wt73 trichosurus
725	2.8	6	166	2	Q9Q5L0	Q9q5l0 herpesvirus	798	6	2.8	182	2	Q6UWJ5	Q6uwj5 homo sapien
726	2.8	6	167	1	RS5_BACCR	Q81j25 bacillus ce	799	6	2.8	182	2	Q9H7Y0	Q9h7y0 homo sapien
727	2.8	6	167	2	Q7MRL1	Q7mr1l wolinnella s	800	6	2.8	182	2	Q8MIP0	Q8mip0 equus cabal
728	2.8	6	168	2	Q9Y8Z0	Q9y8z0 aeropyrum p	801	6	2.8	182	2	Q8GA64	Q8ga64 escherichia
729	2.8	6	168	2	Q6BW24	Q6bw24 debaryomyce	802	6	2.8	182	2	Q8XUF6	Q8xuf6 ralatonia s
730	2.8	6	168	2	Q8IGP0	Q8igp0 drosophila	803	6	2.8	182	2	Q836K0	Q836k0 enterococcu
731	2.8	6	168	2	Q7RNS8	Q7rns8 plasmodium	804	6	2.8	182	2	Q92OK4	Q92ok4 cavia porce
732	2.8	6	168	2	Q6R4W3	Q6r4w3 bacterioph	805	6	2.8	182	2	Q9CUG0	Q9cug0 mus musculu
733	2.8	6	168	2	Q6LAF5	Q6laf5 mus musculu	806	6	2.8	183	1	PSAF_GUITH	Q78457 guillardia
734	2.8	6	168	2	Q9JE54	Q9je54 human immu	807	6	2.8	183	2	Q6NZ44	Q6nz44 homo sapien
735	2.8	6	169	2	Q7QV07	Q7qv07 giardia lam	808	6	2.8	183	2	Q6BFFK4	Q6bffk4 paramecium
736	2.8	6	169	2	Q9RV50	Q9rv50 deinococcus	809	6	2.8	183	2	Q95MP7	Q95mp7 canis fami
737	2.8	6	169	2	Q9RWJ6	Q9rwj6 deinococcus	810	6	2.8	183	2	Q94BT7	Q94bt7 arabidopsis
738	2.8	6	169	2	Q9JE79	Q9je79 human immu	811	6	2.8	183	2	Q6ZHP7	Q6zhp7 oryza sativ
739	2.8	6	170	2	Q7Q086	Q7q086 anopheles g	812	6	2.8	183	2	Q9LI88	Q9li88 arabidopsis
740	2.8	6	170	2	Q947M1	Q947m1 beta vulgar	813	6	2.8	184	2	Q9YCI3	Q9yci3 aeropyrum p
741	2.8	6	170	2	Q84182	Q84182 chlamydia t	814	6	2.8	184	2	Q7QFJ4	Q7qfj4 anopheles g
742	2.8	6	171	2	Q68SU3	Q68su3 pleurotus d	815	6	2.8	184	2	Q9XSG6	Q9xsg6 bos taurus
743	2.8	6	171	2	Q68SU8	Q68su8 pleurotus d	816	6	2.8	184	2	Q98PS7	Q98ps7 mycoplasma
744	2.8	6	171	2	Q81BA7	Q81ba7 bacillus ce	817	6	2.8	184	2	Q830W2	Q830w2 enterococcu
745	2.8	6	171	2	Q9JEB3	Q9je53 human immu	818	6	2.8	184	2	Q640C7	Q640c7 xenopus lae
746	2.8	6	172	2	Q8IL05	Q8il05 plasmodium	819	6	2.8	185	1	FRIH_CRIGR	P29389 cricetulus
747	2.8	6	172	2	Q6ILIA5	Q6ilas drosophila	820	6	2.8	186	1	APL3_GALME	P80703 gallieria me
748	2.8	6	172	2	Q8LIW6	Q8liw6 oryza sativ	821	6	2.8	186	1	THM2_ARATH	Q9seu8 arabidopsis
749	2.8	6	172	2	Q6MCT6	Q6mct6 parachlamyd	822	6	2.8	186	2	Q8ZUQ9	Q8zugu9 pyrobaculum
750	2.8	6	172	2	Q03457	Q03457 feline leuk	823	6	2.8	186	2	Q8LG26	Q8lg26 arabidopsis
751	2.8	6	173	2	Q9B8U8	Q9b8u8 schistosoma	824	6	2.8	186	2	Q6NTR3	Q6ntr3 xenopus lae
752	2.8	6	173	2	Q7ME16	Q7me16 vibrio vuln	825	6	2.8	187	2	Q702D9	Q702d9 uncultured
753	2.8	6	173	2	Q8D3X9	Q8d3x9 vibrio vuln	826	6	2.8	187	2	Q68IJ1	Q68ij1 helicobacte
754	2.8	6	173	2	Q9A9B1	Q9a9b1 caulobacter	827	6	2.8	187	2	Q68IJ1	Q68ij1 helicobacte
755	2.8	6	174	1	RH4A_ARATH	Q84tf5 arabidopsis	828	6	2.8	187	2	Q68IJ2	Q68ij2 helicobacte
756	2.8	6	174	2	Q85594	Q85594 human t-lym	829	6	2.8	187	2	Q68IJ7	Q68ij7 helicobacte
757	2.8	6	176	2	Q81755	Q81755 plasmodium	830	6	2.8	187	2	Q68IJ8	Q68ij8 helicobacte
758	2.8	6	176	2	Q7RK79	Q7rk79 plasmodium	831	6	2.8	187	2	Q68IJ9	Q68ij9 helicobacte
759	2.8	6	176	2	Q7XM27	Q7xm27 oryza sativ	832	6	2.8	187	2	Q68IK0	Q68ik0 helicobacte
760	2.8	6	176	2	Q81H78	Q81h78 bacillus ce	833	6	2.8	187	2	Q68IK1	Q68ik1 helicobacte
761	2.8	6	176	2	Q89TC0	Q89tc0 bradyrhizob	834	6	2.8	187	2	Q68IK2	Q68ik2 helicobacte



835	187	2	681K3	Q68iK3 helicobacte	908	2.8	201	2	Q8Y2R2	Q8y2r2 ralstonia s
836	187	2	Q68IK4	Q68iK4 helicobacte	909	2.8	201	2	Q8FHO	Q8fho rhizobium l
837	187	2	Q68IK5	Q68iK5 helicobacte	910	2.8	202	1	RR4_NEPOL	Q8tkx5 neptroselm
838	187	2	Q68IK6	Q68iK6 helicobacte	911	2.8	202	2	Q64A84	Q64a84 uncultured
839	187	2	Q68IK7	Q68iK7 helicobacte	912	2.8	202	2	Q66I49	Q66i49 homo sapien
840	187	2	Q68IK9	Q68iK9 helicobacte	913	2.8	202	2	Q6AUX7	Q6aux7 oryza sativ
841	187	2	Q68IL0	Q68iL0 helicobacte	914	2.8	202	2	Q6LR08	Q6lr08 photobacter
842	187	2	Q68IL1	Q68iL1 helicobacte	915	2.8	202	2	Q83GI4	Q83gi4 tropheryma
843	187	2	Q68IL2	Q68iL2 helicobacte	916	2.8	202	2	Q83HP6	Q83hp6 tropheryma
844	187	2	Q68IL5	Q68iL5 helicobacte	917	2.8	202	2	Q8S2G6	Q8s2g6 streptomyce
845	187	2	Q68IL6	Q68iL6 helicobacte	918	2.8	202	2	Q82444	Q82444 human t-lym
846	187	2	Q68IL7	Q68iL7 helicobacte	919	2.8	202	2	Q6ER22	Q6erp22 pan troglod
847	187	2	Q68IL8	Q68iL8 helicobacte	920	2.8	203	2	Q6EPW8	Q6epw8 oryza sativ
848	187	2	Q68IL9	Q68iL9 helicobacte	921	2.8	204	1	ALA7_ALTAL	P42058 alternaria
849	187	2	Q68IM1	Q68iM1 helicobacte	922	2.8	204	1	CTF2_MOUSE	P83714 mus musculu
850	187	2	Q68IM4	Q68iM4 helicobacte	923	2.8	204	2	Q8STS1	Q8stsl encephalito
851	187	2	Q68IM6	Q68iM6 helicobacte	924	2.8	204	2	Q7XRT5	Q7xrt5 oryza sativ
852	187	2	Q68IM7	Q68iM7 helicobacte	925	2.8	204	2	Q88IW7	Q88iw7 pseudomonas
853	187	2	Q68IM8	Q68iM8 helicobacte	926	2.8	204	2	Q6R2R3	Q6r2r3 rattus norv
854	187	2	Q68IN0	Q68iN0 helicobacte	927	2.8	205	2	Q7Z2I8	Q7z2i8 homo sapien
855	188	1	RNFB_YERPE	Q8zec9 versinia pe	928	2.8	205	2	Q45046	Q45046 scirpophaga
856	188	2	Q6ZAF2	Q8z8f2 oryza sativ	929	2.8	205	2	Q86AW1	Q86aw1 dictyosteli
857	188	2	Q8P9N4	Q8p9n4 xanthomonas	930	2.8	205	2	Q6F909	Q6f909 acinetobact
858	188	2	Q8PLG1	Q8plg1 xanthomonas	931	2.8	205	2	Q8KI75	Q8ki75 mus musculu
859	188	2	Q882W8	Q882w8 pseudomonas	932	2.8	206	1	PTH_PROMM	Q7v4v4 prochloroco
860	189	2	Q9CAM2	Q9cam2 arabidopsis	933	2.8	206	2	Q8RNX5	Q8rnx5 serratia sp
861	190	2	Q260I9	Q260i9 helicobacte	934	2.8	207	2	Q66AG4	Q66ag4 versinia ps
862	190	2	Q9ZJD4	Q9zjd4 helicobacte	935	2.8	207	2	Q9HX32	Q9hx32 pseudomonas
863	191	2	Q8RSI4	Q8rsi4 uncultured	936	2.8	208	2	Q21506	Q21506 meriones un
864	191	2	Q9QCX2	Q9qcx2 chayote mos	937	2.8	208	2	Q9FLJ31	Q9flj31 arabidopsis
865	192	1	RM11_HUMAN	Q9y3b7 homo sapien	938	2.8	208	2	Q69L68	Q69l68 oryza sativ
866	192	1	RM11_MOUSE	Q9c9f0 mus musculu	939	2.8	208	2	Q8XYN2	Q8xyn2 ralstonia s
867	192	2	Q74N68	Q74n68 nanoarchaeu	940	2.8	208	2	Q7MH18	Q7mh18 vibrio vuln
868	192	2	Q9FUO9	Q9fuq9 oryza mayer	941	2.8	208	2	Q8DCC1	Q8dcl1 vibrio vuln
869	193	2	Q6ZSX6	Q6zsx6 homo sapien	942	2.8	209	2	Q9ZV79	Q9zv79 arabidopsis
870	193	2	Q85MC2	Q85mc2 monoblephar	943	2.8	209	2	Q930U4	Q930u4 rhizobium m
871	193	2	Q8H7G4	Q8h7g4 arabidopsis	944	2.8	209	2	Q68VN7	Q68vn7 rickettsia
872	193	2	Q93J01	Q93j01 streptomyce	945	2.8	210	2	Q9BSE9	Q9bse9 homo sapien
873	194	2	Q6ZNG4	Q6zng4 homo sapien	946	2.8	210	2	Q8MRP3	Q8mrp3 drosophila
874	194	2	Q93YL3	Q93yl3 brassica na	947	2.8	210	2	Q84BA4	Q84ba4 erwinia chr
875	194	2	Q7VB03	Q7vb03 prochloroco	948	2.8	210	2	Q8DXS1	Q8dxs1 streptococc
876	194	2	Q6ARI1	Q6ari1 desulfotale	949	2.8	210	2	Q8E3E1	Q8e3e1 streptococc
877	194	2	Q6HIK8	Q6hiK8 bacillus th	950	2.8	210	2	Q8EGU9	Q8egu9 shewanella
878	195	2	Q6BYJ1	Q6byj1 debaryomyce	951	2.8	211	1	RL4_TREDE	P61070 treponema d
879	195	2	Q72M47	Q72m47 leptospira	952	2.8	211	2	Q6ZQZ3	Q6zqz3 homo sapien
880	195	2	Q8EYM4	Q8eym4 leptospira	953	2.8	211	2	Q7LDF1	Q7ldf1 drosophila
881	196	2	Q9VKF5	Q9vki5 drosophila	954	2.8	211	2	Q7PM91	Q7pm91 anopheles g
882	196	2	Q7MMW3	Q7mmw3 vibrio vuln	955	2.8	211	2	Q9SK58	Q9sk58 macaca fasc
883	196	2	Q87SH6	Q87sh6 vibrio para	956	2.8	211	2	Q9FYZ7	Q9fyz7 nicotiana t
884	196	2	Q8DEJ7	Q8dej7 vibrio vuln	957	2.8	211	2	Q6RGN7	Q6rgn7 streptomyce
885	197	1	CYCL_BACSU	Q34577 bacillus su	958	2.8	211	2	Q7N2V7	Q7nzv7 chromobacte
886	197	2	Q6CG00	Q6cg00 yarrowia li	959	2.8	211	2	Q81QC1	Q81qc1 bacillus an
887	197	2	Q6NUU2	Q6nuj2 homo sapien	960	2.8	212	1	PSAD_SPIOL	P12353 spinacia ol
888	197	2	Q6XU146	Q6xi46 drosophila	961	2.8	212	2	Q7SGR9	Q7sgr9 neurospora
889	197	2	Q8HY68	Q8hy68 macropus fu	962	2.8	212	2	Q04646	Q04646 arabidopsis
890	197	2	Q9STI3	Q9sti3 brassica ca	963	2.8	212	2	Q8LD12	Q8ld12 arabidopsis
891	197	2	Q93L53	Q93l53 bacteroides	964	2.8	212	2	Q9XH35	Q9xh35 oryza sativ
892	197	2	Q6G4S4	Q6g4s4 bartonella	965	2.8	212	2	Q7P2A5	Q7p2a5 fusobacteri
893	197	2	Q7NJA3	Q7nja3 gloeobacter	966	2.8	212	2	Q8RFG2	Q8rfg2 fusobacteri
894	197	2	Q6NXW2	Q6nxw2 mus musculu	967	2.8	212	2	Q74CQ2	Q74cq2 geobacter s
895	197	2	Q6P9V2	Q6p9v2 rattus norv	968	2.8	212	2	Q884R0	Q884r0 pseudomonas
896	198	2	Q9Y3V6	Q9y3v6 homo sapien	969	2.8	212	2	Q89R64	Q89r64 bradyrhizob
897	198	2	Q6MAP7	Q6map7 parachlamyd	970	2.8	214	2	Q9FL33	Q9fl33 pseudomonas
898	199	1	SP25_DROME	Q9vy72 drosophila	971	2.8	214	2	Q92B50	Q92b50 rhizobium m
899	199	2	Q6GOK5	Q6gok5 bartonella	972	2.8	215	2	Q635I8	Q635i8 bacillus ce
900	200	1	TRPG_BUCAI	Q44696 buchnera ap	973	2.8	215	2	Q92YI9	Q92yy9 rhizobium m
901	200	2	Q7SGU7	Q7sgu7 neurospora	974	2.8	215	2	Q73IK5	Q73ik5 bacillus ce
902	200	2	Q81308	Q81308 arabidopsis	975	2.8	215	2	Q81824	Q81824 bacillus ce
903	200	2	Q65HV0	Q65hv0 bacillus li	976	2.8	215	2	Q81MD5	Q81md5 bacillus an
904	201	2	Q8MQ07	Q8mq07 caenorhabdi	977	2.8	215	2	Q6HE74	Q6he74 bacillus th
905	201	2	Q6ZG76	Q6zg76 oryza sativ	978	2.8	216	1	YD82_RHIME	Q2q8d rhizobium m
906	201	2	Q7XBK0	Q7xbk0 papaver nud	979	2.8	216	2	Q6BFR2	Q6bfr2 paramecium
907	201	2	Q25881	Q25881 helicobacte	980	2.8	216	2	Q9N208	Q9n208 callithrix

[illegible]

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DR GO: 0005149; F:interleukin-1 receptor binding; NAS.
DR GO: 0006955; P:immune response; NAS.
DR InterPro: IPR008996; Cytok IL1 like.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR PRINTS: PR00264; INTERLEUKIN1.
DR PRODOM: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; FALSE NEG.
KW Alternative splicing; Cytokine; Direct protein sequencing;
KW Multigene family; Polymorphism.
FT PROPEP 1 45 Removed in mature form.
FT CHAIN 46 218 Interleukin 1 family member 7.
FT VARSPLIC 1 49 MSFVGENSGVKGSEDWEKDEPQCCLDPAGSGPLEPGPSLP
FT TMNFVHTS -> MSGCDRETETKGNKFKRLRG (in isoform A).
FT /FTid=VSP_002653.
FT DPAAGSPLPGPSLPTMNFVHTS -> G (in isoform D).
FT /FTid=VSP_002654.
FT Missing (in isoform E).
FT /FTid=VSP_002655.
FT SPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPE
FT -> K (in isoform C).
FT /FTid=VSP_002656.
FT G -> V.
FT /FTid=VAR_014260.
FT T -> A.
FT /FTid=VAR_014261.
SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;
Query Match 80.7%; Score 176; DB 1; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.6e-172;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 43 MNFVHTSPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPEIFPALSLSAS 102
Db 43 MNFVHTSPKYNLNPFKFSHDQHKVLVDGSLIAVPDKNVIRPEIFPALSLSAS 102
Qy 103 AEKGSPIILGVSGKEFLCYCDKDGQSHPSLQKELKMLAAQKESARRPFIFRAQVG 162
Db 103 AEKGSPIILGVSGKEFLCYCDKDGQSHPSLQKELKMLAAQKESARRPFIFRAQVG 162
Qy 163 SNNMLESAAHPGWFICTSCNENPVGVTDFKFNKHIEFSPQVCKAEMSPSEVSD 218
Db 163 SNNMLESAAHPGWFICTSCNENPVGVTDFKFNKHIEFSPQVCKAEMSPSEVSD 218
RESULT 2
Q7RU00 PRELIMINARY; PRT; 219 AA.
AC Q7RU00
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IL-1F7b (IL-1H4, IL-1H, IL-1RP1).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20545212; PubMed=110931146;
RX DOI=10.1002/1521-4141(200011)30:11<3299::AID-IMMU3299>3.0.CO;2-S;
RA Barton J.L., Herbst R., Bosio D., Higgins L., Nicklin M.J.;
RT "A tissue specific IL-1 receptor antagonist homolog from the IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18 antagonist activities.";
RL Eur. J. Immunol. 30:3299-3308(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97312693; PubMed=9169134; DOI=10.1006/geno.1997.4654;
RX Nothwang H.G., Strahm B., Denich D., Kuebler M., Schwabe J.,
RX Gingrich J.C., Jauch A., Cox A., Nicklin M.J.H., Kurnit D.M.,

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RA Hildebrandt F.;
RT "Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13.";
RT Genomics 41:370-378(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=94245215; PubMed=8188271;
RX Nicklin M.J.H., Weith A., Duff G.W.;
RT "A Physical map of the region encompassing the human interleukin-1-alpha, interleukin-1-beta and interleukin-1 receptor genes.";
RL Genomics 19:382-384(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=2198050; PubMed=11991722; DOI=10.1006/geno.2002.6751;
RX Nicklin M.J.H., Barton J.L., Nguyen M., Fitzgerald M.G., Duff W.G., Kornman K.;
RT "A sequence-based map of the nine genes of the human interleukin-1 cluster.";
RL Genomics 79:718-725(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=99443727; PubMed=10512743; DOI=10.1006/bbrc.1999.1440;
RX Mulero J.J., Pace A.M., Neiken S.T., Loeb D.D., Correa T.R., Drmanac R., Ford J.E.;
RT "IL1H1: A novel interleukin-1 receptor antagonist gene.";
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092889; PubMed=10625660; DOI=10.1074/jbc.275.2.1169;
RX Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garka K.E., Sims J.E.;
RT "Four new members expand the interleukin-1 superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209405; PubMed=10744718; DOI=10.1074/jbc.275.14.10308;
RX Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N., Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L., Young P.R.;
RT "Identification and initial characterization of four novel members of the interleukin-1 family.";
RL J. Biol. Chem. 275:10308-10314(2000).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE=20318623; PubMed=10860666; DOI=10.1006/geno.2000.6184;
RX Busfield S.J., Comrack C.A., Yu G., Chickering T.W., Smucko J.S., Zhou H., Leiby K.R., Holmgren L.M., Gearing D.P., Pan Y.;
RT "Identification and gene organization of three novel members of the IL-1 family on human chromosome 2.";
RL Genomics 66:213-216(2000).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE=21066552; PubMed=11145836; DOI=10.1006/cyto.2000.0799;
RX Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E., Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vanden R.;
RT "IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-1krp.";
RL Cytokine 13:1-7(2001).
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=21282953; PubMed=11278614; DOI=10.1074/jbc.M010095200;
RX Lin H.S., Ho A.S., Haley-Vicente D., Zhang J., Bernal-Fussell J., Pace A.M., Hansen D., Schweighofer K., Mize N.K., Ford J.E.;
RT "Cloning and characterization of IL-1H2, a novel interleukin-1 family member.";
RL J. Biol. Chem. 276:20597-20602(2001).
RN [11]
RP SEQUENCE FROM N.A.
RX MEDLINE=21359532; PubMed=11466363;
RX Debets R., Timans J.C., Homey B., Zurawski S., Sana T.R., Lo S., Wagner J., Edwards G., Clifford T., Menon S., Bazan J.F., Kastelein R.A.;

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RT "Two novel IL-1 family members, IL-1 delta and IL-1 epsilon, function  
as an antagonist and agonist of NF-kB activation through the orphan  
IL-1 receptor-related protein 2.J. Immunol. 167: 1440-1446.";  
RL J. Immunol. 167:1440-1446(2001).  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21459116; PubMed=11574262; DOI=10.1016/S1471-4906(01)02040-3;  
RA Sims J.E., Nicklin M.J., Bazan J.F., Barton J.L., Busfield S.J.,  
Ford J.E., Kastelein R.A., Kumar S., Lin H., Mulero J.J., Pan G.,  
Pan Y., Smith D.E., Young P.R.;  
RT "A new nomenclature for the IL-1-family genes.";  
RL Trends Immunol. 22:536-537(2001).  
CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
EMBL/GenBank/DBJ third party annotation (TPA) entry.  
CC -1- SIMILARITY: CAD29873.1; -.  
DR EMBL; BN000002; CAD29873.1; -.  
DR HSSP; Q9QYI1; IMD6.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005152; F:interleukin-1 receptor antagonist activity; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; CytoK\_IL1like.  
DR InterPro; IPR003297; InterleukinIL1RA.  
DR InterPro; IPR000975; Interleukin\_1.  
DR Pfam; PF00340; IL1; 1.  
DR PRINTS; PR00264; INTERLEUKIN1.  
DR PRINTS; PR01360; INTRLEUKIN1X.  
DR PRODOM; PD002536; Interleukin\_1; 1.  
SQ SEQUENCE 219 AA; 24242 MW; 18EBA0881DF25C41 CRC64;  
  
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Best Local Similarity 100.0%; Pred. No. 7e-48;  
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 109 ILLGVSKGEFLCYCDKQSGHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGS 163  
Db 109 ILLGVSKGEFLCYCDKQSGHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGS 163  
  
RESULT 3  
Q97CB6 PRELIMINARY; PRT; 196 AA.  
ID Q97CB6  
AC Q97CB6  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Hypothetical protein TVG0192051.  
GN Names=TVG0192051; OrderedLocusNames=TV0186;  
OS Thermoplasma volcanium.  
OC Archaea; Euryarchaeota; Thermoplasma; Thermoplasmatales;  
OC Thermoplasmataceae; Thermoplasma.  
OX NCBI\_TaxID=50339;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=GSS1 / DSM 4299 / JCM 9571;  
RC MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;  
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
Kawashima T., Watanabe K., Yamazaki H., Makino K., Kawamoto T.,  
Nunohiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;  
RT "Archaeal adaptation to higher temperatures revealed by genomic  
sequence of Thermoplasma volcanium.";  
Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
RL EMBL; AP000991; BAB59328.1; -.  
DR HSSP; Q9X033; I050.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR000644; CBS.  
DR InterPro; IPR001387; HTH\_3.  
DR InterPro; IPR010982; Lambda\_like\_DNA.  
DR Pfam; PF00571; CBS; 2.  
DR Pfam; PF01381; HTH\_3; 1.  
DR SMART; SM00116; CBS; 2.  
DR SMART; SM00530; HTH\_XRE; 1.  
DR PROSITE; PS00943; HTH\_CROCI1; 1.  
KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 196 AA; 21798 MW; 41132CC5DBBC3CDC CRC64;  
  
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 69 VLVLDSGNL 77  
Db 171 VLVLDSGNL 179  
  
RESULT 4  
Q9SAQ1 PRELIMINARY; PRT; 97 AA.  
ID Q9SAQ1  
AC Q9SAQ1  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE MRP-like ABC transporter (Fragment).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97415407; PubMed=9271206; DOI=10.1016/S0014-5793(97)00702-3;  
RA Tommasini R., Vogt E., Schmid J., Fromentau M., Amrhein N.,  
RA Martinola E.;  
RT "Differential expression of genes coding for ABC transporters after  
treatment of Arabidopsis thaliana with xenobiotics.";  
RL FEBS Lett. 411:206-210(1997).  
DR EMBL; U96398; AAC49796.1; -.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.  
DR GO; GO:0006910; P:transport; IEA.  
DR InterPro; IPR003439; ABC\_transporter.  
DR PRODOM; PD000006; ABC\_transporter; 1.  
FT NON\_TER 1  
FT NON\_TER 97  
SQ SEQUENCE 97 AA; 10774 MW; 80971A33465B2D33 CRC64;  
  
Query Match 3.7%; Score 8; DB 2; Length 97;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 68 KVLVLDSG 75  
Db 51 KVLVLDSG 58  
  
RESULT 5  
Q6ZQY2 PRELIMINARY; PRT; 161 AA.  
ID Q6ZQY2  
AC Q6ZQY2  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein FLJ46805.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=trachea;  
RA Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,  
Tanai H., Watanabe S., Ishida S., Ono Y., Hotuta T., Watanabe M.,  
Sugiyama T., Irie R., Otsuki T., Sato H., Ota T., Wakamatsu A.,  
Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,  
Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,  
Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,

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RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK128646; BAC87547.1; -
DR InterPro; IPR003590; LRR_RNinh_sub.
DR SMART; SMO0368; LRR_RI; 2.
SQ SEQUENCE 161 AA; 17279 MW;  C4643C22000F493 CRC64;

Query Match          3.7%; Score 8; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLSS 100
Db 98 ALASSLSS 105
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RESULT 6
Q87JK9 PRELIMINARY; PRT; 234 AA.
AC Q87JK9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative repressor protein PhnR.
GN OrderedLocusNames=VPA0240;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Nijima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
CC -1- SIMILARITY: Contains 1 HTH gntR-type DNA-binding domain.
DR EMBL; AP005084; BAC61583.1; -
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000524; HTH_GntR
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF00392; GntR; 1.
DR PRINTS; PR00035; HTHGNTR.
DR SMART; SMO0345; HTH_GNTR; 1.
DR PROSITE; PS50949; HTH_GNTR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 234 AA; 27058 MW; 55AF101D68418E9C CRC64;

Query Match          3.7%; Score 8; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 84 NYIRPEIF 91
Db 138 NYIRPEIF 145
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RESULT 7
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AC Q72ME6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Response regulator.
GN OrderedLocusNames=IIC13242;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
```

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OS Copenhageni).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fiocruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.L., Degraeve W.M., Dellagostin O.A., El-Dorzy H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Kuramae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017300; AAS71786.1; -
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR011006; CheY like.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF00072; Response_reg; 1.
DR PRODOM; PD000039; Response_reg; 2.
DR SMART; SMO0448; REC; 2.
DR PROSITE; PS50110; RESPONSE REGULATORY; 2.
KW Complete proteome; Phosphorylation; Sensory transduction.
SQ SEQUENCE 256 AA; 29077 MW; A3A28732218B146B CRC64;

Query Match          3.7%; Score 8; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLDSS 75
Db 2 KVLVLDSS 9
|||||

RESULT 8
Q8EYZ6 PRELIMINARY; PRT; 256 AA.
ID Q8EYZ6
AC Q8EYZ6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Two-component response regulator.
GN OrderedLocusNames=LA4065;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
interrogans revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
DR EMBL; AE011561; AAN51263.1; -
DR HSP; O9A514; 1MB3.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
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DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR InterPro; IPR011006; CheY_like.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF000072; Response_reg; 2.
DR ProDom; PD0000039; Response_reg; 2.
DR SMART; SM00448; REC; 2.
DR PROSITE; PS01110; RESPONSE REGULATORY; 2.
KW Complete proteome; Phosphorylation; Sensory transduction.
SQ SEQUENCE 256 AA; 29104 MW; 3f4f872f280dc689 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 256;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVLDG 75
Db 2 KVLVLDG 9

RESULT 9
ID 073909 PRELIMINARY; PRT; 267 AA.
AC 073909;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-lbета.
GN Names:il-lbета; Synonyms:IL1b;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archoaauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99144128; PubMed=9990317;
RA Weining K.C., Sick C., Kaspers B., Staeheli P.;
RT "A chicken homologue of mammalian interleukin-lbета: cDNA cloning and
purification of active recombinant protein.";
RL Eur. J. Biochem. 258:994-1000(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=line N;
RA Kaiser P., Rothwell L., Goodchild M., Bumstead N.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Produced by activated macrophages, IL-1 stimulates
thymocyte proliferation by inducing IL-2 release, B-cell
maturation and proliferation, and fibroblast growth factor
activity (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the IL-1 family.
DR EMBL; Y15006; CAA75239.1; -.
DR EMBL; AJ245728; CAC04510.1; -.
DR HSSP; P18510; IL1R
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0008283; P:cell proliferation; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006954; P:inflammatory response; IEA.
DR GO; GO:0000074; P:regulation of cell cycle; IEA.
DR InterPro; IPR008996; Cytok_IL1-like.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR003294; InterleukinIL1AB.
DR InterPro; IPR003296; InterleukinIL1B.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PRINTS; PR01359; INTRLEUKIN1B.
DR PRINTS; PR01357; INTRLEUKIN1AB.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.

DR PROSITE; PS00253; INTERLEUKIN 1; 1.
KW Inflammatory response; Mitogen; Pyrogen.
FT CHAIN 106 267 interleukin-lbета.
SQ SEQUENCE 267 AA; 29822 MW; 3EF72164E4D40B64 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 PGWFICT 180
Db 234 PGWFICT 241

RESULT 10
LPSL_RHIME STANDARD; PRT; 341 AA.
ID LPSL_RHIME
AC 054067;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE UDP-glucuronate 5'-epimerase (EC 5.1.3.12) (UDP-glucuronic acid
epimerase).
GN Names:lspL; OrderedLocusNames=R01083; ORFNames=SMC02640;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=984440435; PubMed=9765575;
RA Kereszt A., Kiss E., Reuhs B.L., Carlson R.W., Kondorosi A.,
Putnoky P.;
RT "Novel rkp gene clusters of Sinorhizobium meliloti involved in
capsular polysaccharide production and invasion of the symbiotic
nodule: the rkp gene encodes a UDP-glucose dehydrogenase.";
RL J. Bacteriol. 180:5426-5431(1998).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
Boistard P., Becker A., Roury M., Cadieu E., Dreano S., Gloux S.,
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
Pohl T., Portecelle D., Puehler A., Purnelle B., Ramsperger U.,
Renard C., Thebaud P., Vandenbol M., Weidner S., Galibert F.;
RA "Analysis of the chromosome sequence of the legume symbiont
Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- CATALYTIC ACTIVITY: UDP-D-glucuronate = UDP-L-iduronate.
CC -1- COFACTOR: NAD.
CC -1- SIMILARITY: Belongs to the sugar epimerase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; AJ222661; CAA10917.1; -.
DR EMBL; AL591786; CAC45662.1; -.
DR PIR; T46572; T46572.
DR InterPro; IPR001509; Epimerase Dh.
DR InterPro; IPR008089; Nuc_sugar_epim.
DR Pfam; PF01370; Epimerase_1.
DR PRINTS; PR01713; NUCEPIMERASE.
KW Complete proteome; Isomerase; NAD.
FT CONFLICT 176 176 S -> A (in Ref. 1).
SQ SEQUENCE 341 AA; 38098 MW; D678ED2EAFD89395 CRC64;
```

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Query Match 3.7%; Score 8; DB 1; Length 341;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 161 VGSNNMLE 168
Db 105 VGSNNMLE 112

RESULT 11
PDK4 MOUSE
ID PDK4_MOUSE STANDARD; PRT; 412 AA.
AC 070571;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE [Pyruvate dehydrogenase (lipoamide)] kinase isozyme 4, mitochondrial
DE precursor (EC 2.7.1.99) (Pyruvate dehydrogenase kinase isoform 4).
GN Name=Pdk4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H; TISSUE=Heart;
RA Horiuchi M., Kobayashi K., Masuda M., Saheki T.;
RT "A novel gene in carnitine-deficient JVS mice";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Jeoung N.H., Bowker-Kinley M.M., Harris R.A.;
RT "Promoter and partial structural region of Mus musculus pyruvate
dehydrogenase kinase 4 (PDK4).";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fehey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinnow J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Inhibits the mitochondrial pyruvate dehydrogenase
complex by phosphorylation of the E1 alpha subunit, thus
contributing to the regulation of glucose metabolism (By
similarity).
CC -!- CATALYTIC ACTIVITY: ATP + [pyruvate dehydrogenase (lipoamide)] =
ADP + [pyruvate dehydrogenase (lipoamide)] phosphate.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -!- SIMILARITY: Belongs to the PKB/BCKDK protein kinase family.
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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CC EMBL; AJ001418; CAA04752.1; -
CC EMBL; AF239176; AAG44393.1; -
CC EMBL; BC026134; AAH26134.1; -
CC HSSP; Q64536; 1JW6.
CC MGD; MGI:1351481; Pdk4.
CC InterPro; IPR003594; ATPbind_ATPase.
CC InterPro; IPR004358; Bact_sense_pr_C.
CC InterPro; IPR005467; His_Kinase.
CC Pfam; PF02518; HATPase_C; 1.
CC PRINTS; PR00344; BCTRLSENSOR.
CC SMART; SM00387; HATPase_C; 1.
CC PROSITE; PS50109; HIS_KIN; 1.
KW Kinase; Mitochondrion; Multigene family; Phosphorylation; Transferase;
KW TRANSIT peptide.
FT CHAIN ? 1 ? Mitochondrion (Potential).
FT [Pyruvate dehydrogenase (lipoamide)]
FT kinase isozyme 4.
FT DOMAIN 138 368 Histidine kinase.
FT MOD_RES 127 127 Phosphohistidine (by autocatalysis) (By
similarity).
FT SEQUENCE 412 AA; 46596 MW; 74815502E711054C CRC64;

Query Match 3.7%; Score 8; DB 1; Length 412;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 ASSLSAS 102
Db 11 ASSLSAS 18

RESULT 12
Q9YCD8
ID Q9YCD8 PRELIMINARY; PRT; 413 AA.
AC Q9YCD8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein APEL1319.
GN OrderedLocNames=APEL1319;
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococccaceae; Aeropyrum.
OX NCBI_TaxID=56636;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hirao Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101 (1999).
DR EMBL; AP000061; BAA80310.1; -
DR PIR; H72606; H72606.
DR InterPro; IPR002881; DUF58.
DR Pfam; PF01882; DUF58; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 413 AA; 44385 MW; 3CE488692B58A2BD CRC64;

Query Match 3.7%; Score 8; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 94 LASSLSSA 101
Db 12 LASSLSSA 19
|||||

RESULT 13
Q9UEU4 PRELIMINARY; PRT; 595 AA.
AC Q9UEU4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Imidazoline receptor antisera-selected protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9066883; PubMed=9851558; DOI=10.1016/S0165-1838(98)00094-0;
RA Ivanov T.R., Jones J.C., Döntenwill M., Bousquet P., Piletz J.E.;
RT "Characterization of a partial cDNA clone detected by imidazoline
RT receptor-selective antisera.";
RL J. Auton. Nerv. Syst. 72:98-110(1998).
DR EMBL: AF058290; AAC33321.1; -.
DR GO: GO:0004872; P:receptor activity; IEA.
DR InterPro: IPR001128; Cytochrome_P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
KW Receptor.
FT NON_TER 1
FT NON_TER 595
FT NON_TER 595
SQ SEQUENCE 595 AA; 65354 MW; 93139B536F447CDB CRC64;

Query Match 3.7%; Score 8; DB 2; Length 595;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 ALASSLSS 100
Db 50 ALASSLSS 57
|||||

RESULT 14
Q8RX76 PRELIMINARY; PRT; 787 AA.
AC Q8RX76;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE A1930400/T4K22.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL: AY090258; AAL90919.1; -.
DR HSP; Q9CHL6; LMV5.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO: GO:0000166; F:nucleotide binding; IEA.

GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR011527; ABC_membrane_1.
DR InterPro: IPR001140; ABC_TM_transp.
DR InterPro: IPR003439; ABC_transporter.
DR Pfam: PF00664; ABC_membrane_1.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00929; ABC_TMIF; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding.
SQ SEQUENCE 787 AA; 87774 MW; 4D3532D4BAADD469 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 68 KVLVLDGS 75
Db 605 KVLVLDGS 612
|||||

RESULT 15
Q7SE30 PRELIMINARY; PRT; 931 AA.
AC Q7SE30;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU02764.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Quid D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitremikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Newes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Herglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AABX01000039; EAA35023.1; -.
DR InterPro: IPR000219; RHOGEF.
DR Pfam: PF00621; RHOGEF; 1.
DR PROSITE; PS00040; DH2; 1.
SQ SEQUENCE 931 AA; 103386 MW; C7F61C7B91B02567 CRC64;

Query Match 3.7%; Score 8; DB 2; Length 931;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 LASSLSSA 101
Db 433 LASSLSSA 440
|||||

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Search completed: October 13, 2005, 18:59:22  
Job time : 231 secs

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OM protein - protein search, using sw model

Run on: October 13, 2005, 18:47:57 ; Search time 16 Seconds  
(without alignments)  
1310.953 Million cell up

Title: US-10-694-978-4  
 Perfect score: 218  
 Sequence: 1 MSFVGENSGVKMGSEDWEKD.....IEFSQPVCKAENSPSEVSD 218

Scoring table: OLIGO .  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6

Total number of hits satisfying chosen parameters: 943

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Listing first 1000 summaries

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Database : PIR 79:*
1: pir1:
2: pir2:
3: pir3:
4: pir4:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	8	3.7	341	2	T46572	probable UDP-glucose 4-epimerase
2	8	3.7	413	2	H72606	hypothetical protein
3	8	3.7	982	2	T06576	probable protein kinase
4	8	3.7	993	2	T17230	hypothetical protein
5	8	3.7	1427	2	T32219	atp-binding cassette
6	8	3.7	1622	2	D86428	glutathione S-conjugase
7	8	3.7	2118	2	T13612	hypothetical protein
8	7	3.2	116	2	E72509	probable non specific
9	7	3.2	130	2	F72531	hypothetical protein
10	7	3.2	132	2	F96779	probable ribosomal
11	7	3.2	133	2	F71189	hypothetical protein
12	7	3.2	134	2	E64375	hypothetical protein
13	7	3.2	178	2	JE0264	cyclin I - human
14	7	3.2	185	2	T49611	hypothetical protein
15	7	3.2	208	2	T52450	ribosomal protein
16	7	3.2	240	2	C83702	transcription regulator
17	7	3.2	265	2	T42957	hypothetical protein
18	7	3.2	279	2	B89849	prolipoprotein diacylglycerol
19	7	3.2	290	2	H90001	lipoprotein precursor
20	7	3.2	301	2	T18788	hypothetical protein
21	7	3.2	307	2	F69898	hypothetical protein
22	7	3.2	356	2	T70025	multidrug-efflux transporter
23	7	3.2	366	2	T26038	hypothetical protein
24	7	3.2	382	2	F82428	iron-containing alcohol
25	7	3.2	421	2	T02135	hypothetical protein
26	7	3.2	444	2	A11854	hypothetical protein
27	7	3.2	466	2	E97252	fof1-type ATP synthase
28	7	3.2	506	2	A40679	transcription enhancer
29	7	3.2	523	2	B40679	transcription enhancer

103	6	2.8	145	2	S76877	hypothetical prote	176	6	2.8	178	1	LGBO	beta-lactoglobulin
104	6	2.8	146	1	HBFTF	hemoglobin beta ch	177	6	2.8	178	2	C71524	hypothetical prote
105	6	2.8	146	1	HBEM	hemoglobin beta ch	178	6	2.8	180	1	LGST	beta-lactoglobulin
106	6	2.8	146	1	HBFXB	hemoglobin beta ch	179	6	2.8	180	1	LGSH	beta-lactoglobulin
107	6	2.8	146	1	HBGP	hemoglobin beta ch	180	6	2.8	180	2	A26886	ferritin heavy cha
108	6	2.8	146	1	HBHY	hemoglobin beta ch	181	6	2.8	181	2	S69721	probable adenine p
109	6	2.8	146	1	HBMN1	hemoglobin beta mi	182	6	2.8	181	2	A39884	ferritin heavy cha
110	6	2.8	146	1	HBOE	hemoglobin beta ch	183	6	2.8	182	2	S06070	ferritin heavy cha
111	6	2.8	146	1	HBTSM	hemoglobin beta ch	184	6	2.8	183	1	FRUHH	ferritin heavy cha
112	6	2.8	146	1	HBOY	hemoglobin beta ch	185	6	2.8	184	2	B90592	hypothetical prote
113	6	2.8	146	1	HGBAY	hemoglobin gamma c	186	6	2.8	184	2	B72601	hypothetical prote
114	6	2.8	146	1	HGMQJ	hemoglobin gamma c	187	6	2.8	186	2	F85044	probable M-type th
115	6	2.8	146	1	HGMOP	hemoglobin gamma c	188	6	2.8	186	2	S11569	hypothetical prote
116	6	2.8	146	2	A34947	hemoglobin beta ch	189	6	2.8	186	2	T72228	ornithine decarbox
117	6	2.8	146	2	B29392	hemoglobin beta ch	190	6	2.8	186	2	T09296	apolipoprotein III
118	6	2.8	146	2	B29391	hemoglobin beta ch	191	6	2.8	188	2	AG0273	probable iron-sulf
119	6	2.8	146	2	B25729	hemoglobin beta ch	192	6	2.8	188	2	G96657	hypothetical prote
120	6	2.8	146	2	B25359	hemoglobin beta ch	193	6	2.8	189	2	G96657	conserved hypotet
121	6	2.8	146	2	B24690	hemoglobin beta-S	194	6	2.8	190	1	E64705	hypothetical prote
122	6	2.8	146	2	SU0163	PTS fructose-speci	195	6	2.8	190	2	E71815	hypothetical prote
123	6	2.8	146	2	S11398	hemoglobin gamma-G	196	6	2.8	192	2	S53555	probable membrane
124	6	2.8	147	1	I37025	hemoglobin beta ma	197	6	2.8	192	2	C69677	adenylsulfate ki
125	6	2.8	147	1	HBM5	hemoglobin beta-II	198	6	2.8	198	2	T08740	hypothetical prote
126	6	2.8	147	1	HBT	hemoglobin beta-II	199	6	2.8	200	2	T01335	hypothetical prote
127	6	2.8	147	1	HGCG	hemoglobin epsilon	200	6	2.8	201	2	B64685	hypothetical prote
128	6	2.8	147	1	HGTL	hemoglobin epsilon	201	6	2.8	202	2	T36138	hypothetical prote
129	6	2.8	147	1	HMSY2	hemoglobin epsilon	202	6	2.8	204	1	S43111	minor allergen - A
130	6	2.8	147	1	HGCZA	hemoglobin gamma-A	203	6	2.8	206	2	B48441	antigen (C-fermina
131	6	2.8	147	1	HGCZG	hemoglobin gamma-G	204	6	2.8	207	2	F83148	hypothetical prote
132	6	2.8	147	1	HGCC	hemoglobin gamma c	205	6	2.8	209	2	F84482	hypothetical prote
133	6	2.8	147	1	HGHUA	hemoglobin gamma-A	206	6	2.8	209	2	D95274	hypothetical prote
134	6	2.8	147	1	HGHUG	hemoglobin gamma-G	207	6	2.8	212	1	A1SP2	photosystem I chai
135	6	2.8	147	1	HGMQR	hemoglobin gamma-1	208	6	2.8	212	2	T01795	hypothetical prote
136	6	2.8	147	1	HGMQR2	hemoglobin gamma-2	209	6	2.8	215	2	C95352	hypothetical prote
137	6	2.8	147	1	I37022	hemoglobin gamma-A	210	6	2.8	218	2	G86758	DNA-(apurinic or a
138	6	2.8	147	2	I77303	hemoglobin gamma c	211	6	2.8	220	2	E72210	hypothetical prote
139	6	2.8	147	2	I77302	hemoglobin epsilon	212	6	2.8	221	2	AG1066	hypothetical prote
140	6	2.8	147	2	A42829	hemoglobin epsilon	213	6	2.8	221	2	T17997	hypothetical prote
141	6	2.8	147	2	A30213	hemoglobin epsilon	214	6	2.8	222	2	A81944	hypothetical prote
142	6	2.8	147	2	I84437	hemoglobin epsilon	215	6	2.8	224	2	T39158	hypothetical prote
143	6	2.8	147	2	A49402	hemoglobin epsilon	216	6	2.8	225	2	H75571	lysophospholipase
144	6	2.8	147	2	I37011	hemoglobin epsilon	217	6	2.8	225	2	B83505	conserved hypotet
145	6	2.8	147	2	I77304	hemoglobin gamma c	218	6	2.8	227	2	H97336	hypothetical prote
146	6	2.8	147	2	B42829	hemoglobin gamma c	219	6	2.8	228	2	C71435	uncharacterized co
147	6	2.8	147	2	I37036	hemoglobin gamma-2	220	6	2.8	229	2	E70978	probable enoyl-CoA
148	6	2.8	147	2	I37035	hemoglobin gamma-1	221	6	2.8	229	2	S25964	hypothetical prote
149	6	2.8	147	2	I37002	hemoglobin gamma c	222	6	2.8	230	2	T20959	hypothetical prote
150	6	2.8	147	2	A27800	hemoglobin gamma-1	223	6	2.8	234	2	T17550	hypothetical prote
151	6	2.8	147	2	I37020	hemoglobin epsilon	224	6	2.8	234	2	F82440	probable repressor
152	6	2.8	147	2	S00840	hemoglobin beta ch	225	6	2.8	235	2	AG3636	proteinase I (BC 3
153	6	2.8	147	2	A25747	hemoglobin beta II	226	6	2.8	237	2	AD0084	MoTA/ToIQ/ExbB pro
154	6	2.8	148	2	I77330	hemoglobin gamma c	227	6	2.8	237	2	C83689	hypothetical prote
155	6	2.8	150	1	NNEB1C	anthranilate synth	228	6	2.8	241	2	E91294	hypothetical prote
156	6	2.8	152	1	ZBBP74	gene 57B protein -	229	6	2.8	241	2	H86135	probable regulator
157	6	2.8	153	2	H86034	hypothetical prote	230	6	2.8	241	2	S56592	probable regulator
158	6	2.8	153	2	G91187	hypothetical prote	231	6	2.8	241	2	B71128	hypothetical 27K p
159	6	2.8	153	2	S47817	hypothetical 18.1K	232	6	2.8	242	2	D81161	conserved hypotet
160	6	2.8	154	2	F86306	F20D23.22 protein	233	6	2.8	242	2	F48581	hypothetical prote
161	6	2.8	155	4	S21403	hemoglobin gamma-G	234	6	2.8	246	2	F84412	oxidoreductase lim
162	6	2.8	158	1	D69266	hypothetical prote	235	6	2.8	246	2	AB0261	hypothetical phage
163	6	2.8	158	2	H82210	probable acetyltra	236	6	2.8	248	2	A29624	spherulin la precu
164	6	2.8	162	1	LGBU1	beta-lactoglobulin	237	6	2.8	248	2	AH3575	surface protein [i
165	6	2.8	162	2	S00132	beta-lactoglobulin	238	6	2.8	250	2	F95218	hypothetical prote
166	6	2.8	164	2	I46710	ferritin heavy cha	239	6	2.8	250	2	D98082	hypothetical prote
167	6	2.8	164	2	T16168	hypothetical prote	240	6	2.8	251	2	B64337	hypothetical prote
168	6	2.8	166	2	T48040	hypothetical prote	241	6	2.8	252	2	H83390	hypothetical prote
169	6	2.8	168	2	F72481	hypothetical prote	242	6	2.8	253	2	D88338	protein F15A4.5 [i
170	6	2.8	169	2	C75427	hypothetical prote	243	6	2.8	253	2	E72302	esterase - Thermot
171	6	2.8	169	2	B75490	hypothetical prote	244	6	2.8	253	2	T17312	hypothetical prote
172	6	2.8	170	2	B71548	hypothetical prote	245	6	2.8	253	2	G81389	probable DNA-direc
173	6	2.8	173	2	G87383	acetyltransferase,	246	6	2.8	254	2	E97358	inner membrane pro
174	6	2.8	173	2	C84684	hypothetical prote	247	6	2.8	254	2	E75052	guFA protein homol
175	6	2.8	174	2	A41358	gag polyprotein -	248	6	2.8	256	2	C96937	chemotaxis motilit

249	6	2.8	259	1	B64251	probable methyltra	322	6	2.8	300	2	S73528	probable lipoprote
250	6	2.8	259	2	F70032	ABC transporter (A	323	6	2.8	300	2	T29112	hypothetical prote
251	6	2.8	261	2	S63604	homeobox protein G	324	6	2.8	302	2	F75619	hypothetical hemin ABC
252	6	2.8	262	1	A31372	granzyme A (EC 3.4	325	6	2.8	303	2	E81348	binding-protein de
253	6	2.8	264	2	H71804	ribosomal protein	326	6	2.8	304	2	S59414	hypothetical prote
254	6	2.8	264	2	B64714	ribosomal protein	327	6	2.8	305	2	C85042	SIR1-like syntxin
255	6	2.8	264	2	E95410	probable ABC trans	328	6	2.8	305	2	T47521	asparaginase (EC 3
256	6	2.8	266	2	H82387	glucosamine-6-phos	329	6	2.8	305	2	A75234	hypothetical prote
257	6	2.8	266	2	F97259	dinucleotide-utili	330	6	2.8	305	2	A71247	probable L-asparag
258	6	2.8	266	2	F90056	conserved hypotet	331	6	2.8	306	2	A72668	probable spermidin
259	6	2.8	267	2	H83426	3'-phosphoadenosin	332	6	2.8	306	2	A86407	unknown protein [i
260	6	2.8	267	1	D83CEP	DNA-formamidopyrim	333	6	2.8	307	2	C97404	hypothetical prote
261	6	2.8	269	2	AG0971	formamidopyrimidin	334	6	2.8	307	2	S62472	probable Methylthi
262	6	2.8	269	2	G86039	formamidopyrimidin	335	6	2.8	307	2	E38448	acyltransferase (E
263	6	2.8	269	2	F91192	formamidopyrimidin	336	6	2.8	307	2	S11686	acyltransferase (E
264	6	2.8	270	2	F64050	glucosamine-6-phos	337	6	2.8	307	2	F87389	transcription regu
265	6	2.8	270	2	T43039	hypothetical prote	338	6	2.8	309	2	B84550	hypothetical prote
266	6	2.8	271	2	G87071	hypothetical prote	339	6	2.8	310	2	T39024	probable eukaryoti
267	6	2.8	271	2	T18056	ATPase homolog A55	340	6	2.8	311	2	T38934	hypothetical prote
268	6	2.8	271	2	B86918	hypothetical prote	341	6	2.8	313	2	G86336	hypothetical prote
269	6	2.8	271	2	S12560	transcription fact	342	6	2.8	314	2	T15045	spermidine synthas
270	6	2.8	272	2	G71115	hypothetical prote	343	6	2.8	314	2	S52223	hypothetical prote
271	6	2.8	273	1	E64625	hydroxyethylthiaz	344	6	2.8	314	2	T03524	cobD protein - Rho
272	6	2.8	273	2	AC0294	Conserved hypotet	345	6	2.8	314	2	A36195	developmental prot
273	6	2.8	274	2	G70653	probable glpQ1 pro	346	6	2.8	314	2	A41544	developmental prot
274	6	2.8	275	2	F71714	2-dehydro-3-deoxyp	347	6	2.8	315	1	K1EBRT	ribose-phosphate d
275	6	2.8	276	2	S56696	narbonin (clone pN	348	6	2.8	315	1	K1ECRY	ribose-phosphate d
276	6	2.8	276	2	S74745	ABC-type transport	349	6	2.8	315	2	E85700	phosphoribosylpyro
277	6	2.8	277	1	Q0ECAD	probable membrane	350	6	2.8	315	2	AF0720	ribose-phosphate d
278	6	2.8	277	2	I47162	Ig gamma 4 chain c	351	6	2.8	315	2	H90842	phosphoribosylpyro
279	6	2.8	277	2	AC0704	conserved hypotet	352	6	2.8	315	2	AG0245	ribose-phosphate d
280	6	2.8	277	2	F85778	hypothetical prote	353	6	2.8	315	2	E83369	probable transcrip
281	6	2.8	277	2	B90930	hypothetical prote	354	6	2.8	315	2	T42682	hypothetical prote
282	6	2.8	277	2	D82392	conserved hypotet	355	6	2.8	317	2	G82635	methanol dehydroge
283	6	2.8	279	2	S73526	probable lipoprote	356	6	2.8	320	2	G88989	protein C36C5.8 [i
284	6	2.8	279	2	S75552	hypothetical prote	357	6	2.8	321	2	A84792	hypothetical prote
285	6	2.8	279	2	H87917	protein F28D9.1 [i	358	6	2.8	322	2	C82293	riboflavin kinase/
286	6	2.8	279	2	B72481	hypothetical prote	359	6	2.8	325	2	T25331	hypothetical prote
287	6	2.8	280	2	S47815	hypothetical 31.8K	360	6	2.8	325	2	S65306	hypothetical prote
288	6	2.8	280	2	F86034	hypothetical prote	361	6	2.8	326	2	S28706	hypothetical prote
289	6	2.8	280	2	H75151	abc transporter, A	362	6	2.8	327	2	B75341	probable oxidoredu
290	6	2.8	281	2	S08410	probable transcrip	363	6	2.8	328	2	I47160	Ig gamma 2b chain
291	6	2.8	281	2	S18541	hypothetical prote	364	6	2.8	328	2	I47161	Ig gamma 3 chain c
292	6	2.8	283	2	T31122	probable transcrip	365	6	2.8	328	2	I47158	Ig gamma 1 chain c
293	6	2.8	283	2	S73524	probable lipoprote	366	6	2.8	328	2	I47159	Ig gamma 2a chain
294	6	2.8	283	2	S73523	probable lipoprote	367	6	2.8	329	2	D72669	hypothetical prote
295	6	2.8	284	2	AC2622	hypothetical prote	368	6	2.8	329	2	S63135	hypothetical prote
296	6	2.8	284	2	AB1343	transcription regu	369	6	2.8	329	2	T65768	smooth muscle myos
297	6	2.8	284	2	D81075	conserved hypotet	370	6	2.8	330	2	A75480	lipoic acid syntha
298	6	2.8	284	2	D81866	hypothetical prote	371	6	2.8	331	2	F85873	cell division prot
299	6	2.8	284	2	AF2491	hypothetical prote	372	6	2.8	331	2	E91029	cell division prot
300	6	2.8	284	2	AF1713	transcription regu	373	6	2.8	331	2	G65004	Div protein - Esch
301	6	2.8	284	2	G71132	probable cobalt tr	374	6	2.8	331	2	A75323	probable chromosom
302	6	2.8	285	2	S49880	hypothetical narbo	375	6	2.8	331	2	H90576	lipoprotein d limp
303	6	2.8	285	2	T51576	hypothetical prote	376	6	2.8	332	2	WZBYR	arginase (EC 3.5.3
304	6	2.8	289	1	S72862	cysQ homolog - Myc	377	6	2.8	333	1	T37871	hypothetical nucle
305	6	2.8	289	2	A83656	hypothetical prote	378	6	2.8	333	2	T36449	hypothetical prote
306	6	2.8	290	2	F90332	hypothetical prote	379	6	2.8	334	1	RDECEP	N-acetyl-gamma-glu
307	6	2.8	290	2	A93371	hypothetical prote	380	6	2.8	334	2	F86372	hypothetical prote
308	6	2.8	290	2	T09363	hypothetical prote	381	6	2.8	334	2	A39605	transcription regu
309	6	2.8	291	2	S56697	narbonin (clone pN	382	6	2.8	334	1	KHRTL	cathepsin L (EC 3.
310	6	2.8	291	2	S56698	narbonin (clone pN	383	6	2.8	334	2	AB0936	N-acetyl-gamma-glu
311	6	2.8	292	2	T49261	hypothetical prote	384	6	2.8	334	2	G91239	N-acetyl-gamma-glu
312	6	2.8	293	2	B90159	porphobilinogen de	385	6	2.8	334	2	D86087	N-acetyl-gamma-glu
313	6	2.8	295	2	T51350	RNA helicase RH31	386	6	2.8	334	2	F86372	Spermidine synthas
314	6	2.8	295	4	S36174	RNA binding protei	387	6	2.8	334	2	A39605	transcription regu
315	6	2.8	296	2	I52860	smooth muscle myos	388	6	2.8	335	2	T21503	hypothetical prote
316	6	2.8	296	2	AD0467	probable membrane	389	6	2.8	336	2	E75040	hydrogenase expres
317	6	2.8	296	2	H83480	cytochrome o ubiqu	390	6	2.8	336	2	D71121	probable hydrogena
318	6	2.8	296	2	G97799	hypothetical prote	391	6	2.8	336	2	G95003	membrane protein [
319	6	2.8	298	2	T09975	H <sub>2</sub> -transporting tw	392	6	2.8	337	1	WMBE32	ribonucleoside-dip
320	6	2.8	298	2	F90495	conserved hypotet	393	6	2.8	337	1	WMBE32	ribonucleoside-dip
321	6	2.8	300	2	G95954	probable dTDP-4-de	394	6	2.8	337	2	C36953	acetoin[2,6-dichlo

395	6	2.8	339	2	B89878	hypothetical prote	468	6	2.8	408	2	T02133	hypothetical prote
396	6	2.8	340	2	T01492	spermidine synthas	469	6	2.8	409	2	C82036	multidrug resistan
397	6	2.8	340	2	F75193	asparaginase (EC 3	470	6	2.8	410	2	S44626	C503.8 protein -
398	6	2.8	340	2	B97876	conserved hypotet	471	6	2.8	410	2	D98177	hypothetical prote
399	6	2.8	341	2	T31826	hypothetical prote	472	6	2.8	411	2	C64052	NADH2 dehydrogen
400	6	2.8	341	2	S40612	myosin-related pro	473	6	2.8	412	2	H87281	thiolase family pr
401	6	2.8	341	2	AG2880	ABC transporter, s	474	6	2.8	412	2	S07537	myosin heavy chain
402	6	2.8	341	2	G97856	conserved hypotet	475	6	2.8	413	2	S61305	cycH protein - Par
403	6	2.8	342	2	T22742	hypothetical prote	476	6	2.8	413	2	A10598	probable phospholi
404	6	2.8	343	2	AG1273	N-acetylglutamate	477	6	2.8	413	2	AF1427	an hypothetical pr
405	6	2.8	343	2	T08442	hypothetical prote	478	6	2.8	414	2	AI2544	hypothetical prote
406	6	2.8	344	2	A72780	probable ribosomal	479	6	2.8	415	2	A35560	lysosomal membrane
407	6	2.8	345	2	AG3186	hypothetical prote	480	6	2.8	416	2	G84108	cell wall lytic ac
408	6	2.8	345	2	S51548	killer toxin K28 -	481	6	2.8	417	2	B71034	hypothetical prote
409	6	2.8	345	2	AE2914	conserved hypotet	482	6	2.8	418	2	AE2965	exopolysaccharide
410	6	2.8	345	2	H97688	hypothetical prote	483	6	2.8	418	2	H98317	exopolysaccharide
411	6	2.8	346	2	S56665	tryptophan synthas	484	6	2.8	419	2	I38024	MITF protein - hum
412	6	2.8	347	2	D84333	alcohol dehydrogen	485	6	2.8	419	2	A40728	microphthalma-ass
413	6	2.8	348	2	A57234	lin-44 protein pre	486	6	2.8	419	2	C40901	hypothetical prote
414	6	2.8	348	2	S57601	ribonuclease H (EC	487	6	2.8	420	2	B97843	hypothetical prote
415	6	2.8	348	2	T29515	hypothetical prote	488	6	2.8	421	2	B82062	glycine hydroxymet
416	6	2.8	349	2	S74439	iron(III) dicitrat	489	6	2.8	421	2	F0M0GC	conserved hypotet
417	6	2.8	349	2	B99420	hypothetical prote	490	6	2.8	426	2	T06086	gag polyprotein -
418	6	2.8	351	2	T40854	hypothetical prote	491	6	2.8	426	2	C75297	probable protein s
419	6	2.8	352	2	T04841	protein kinase hom	492	6	2.8	427	1	C64408	hypothetical prote
420	6	2.8	352	2	T25170	hypothetical prote	493	6	2.8	429	1	F0LJCN	gag polyprotein -
421	6	2.8	356	2	T19015	hypothetical prote	494	6	2.8	429	1	F0LJGH	probable gag poly
422	6	2.8	356	2	AH1881	hypothetical prote	495	6	2.8	429	2	S06073	gag polyprotein -
423	6	2.8	357	2	A95888	probable ABC trans	496	6	2.8	429	2	T22495	hypothetical prote
424	6	2.8	360	2	F69342	DNA primase homolo	497	6	2.8	431	2	H82237	histidinol dehydro
425	6	2.8	361	2	A40023	paired box homolog	498	6	2.8	431	2	T46187	polygalacturonase
426	6	2.8	364	2	T35353	hypothetical prote	499	6	2.8	432	2	T23762	hypothetical prote
427	6	2.8	365	2	T28184	hypothetical prote	500	6	2.8	434	2	G95124	GTP-binding protei
428	6	2.8	367	2	A83681	ABC transporter (p	501	6	2.8	435	2	T15737	hypothetical prote
429	6	2.8	369	2	H82357	tRNA (uracil-5-)-m	502	6	2.8	435	2	T19687	hypothetical prote
430	6	2.8	370	1	B43673	chloromuconate cyc	503	6	2.8	436	2	A37953	transcription regu
431	6	2.8	370	2	AH2161	cobalamn biosynth	504	6	2.8	436	2	H97594	GTP-binding protei
432	6	2.8	370	2	S75625	hypothetical prote	505	6	2.8	436	2	G71862	alpha-(1,3)-fucosy
433	6	2.8	370	2	T32615	hypothetical prote	506	6	2.8	437	2	F70114	probable zinc prot
434	6	2.8	371	2	F83487	hypothetical prote	507	6	2.8	437	2	B53193	hedghehog homolog v
435	6	2.8	371	2	B84709	hypothetical prote	508	6	2.8	441	2	JC7653	pectate lyase (EC
436	6	2.8	372	2	T17474	chalcone synthase	509	6	2.8	441	2	E72579	hypothetical prote
437	6	2.8	372	2	T23680	hypothetical prote	510	6	2.8	441	2	C95307	probable transport
438	6	2.8	372	2	I49008	melanocortin-5, rec	511	6	2.8	442	2	F71930	probable transport
439	6	2.8	373	2	D71428	cysteine proteinas	512	6	2.8	442	2	A64582	sodium- and chlori
440	6	2.8	377	2	C88930	protein RliG11.9 [	513	6	2.8	444	2	E69102	GDP dissociation i
441	6	2.8	378	2	T19012	hypothetical prote	514	6	2.8	445	2	A56024	GDP dissociation i
442	6	2.8	380	2	C84710	hypothetical prote	515	6	2.8	445	2	C56956	rab GDP dissociati
443	6	2.8	382	2	D70587	probable dnaJ2 pro	516	6	2.8	445	2	B54091	protein F20N2.10 [
444	6	2.8	382	2	T49724	hypothetical prote	517	6	2.8	445	2	A96599	hypothetical prote
445	6	2.8	385	2	E83414	conserved hypotet	518	6	2.8	446	2	D71418	amino acid transpo
446	6	2.8	387	2	B75211	multidrug resistan	519	6	2.8	446	2	H90507	hypothetical prote
447	6	2.8	387	2	H72862	hypothetical prote	520	6	2.8	446	2	F86815	gene A protein - y
448	6	2.8	387	2	T41844	AcMNPV orf103 - Bo	521	6	2.8	447	2	S28086	probable two-compo
449	6	2.8	387	2	B71247	hypothetical prote	522	6	2.8	447	2	C82958	glycerol dehydroge
450	6	2.8	389	2	T38455	hypothetical prote	523	6	2.8	450	2	T37628	glucoamylase precu
451	6	2.8	389	2	E95422	probable transmemb	524	6	2.8	450	2	T39433	flagellar hook-len
452	6	2.8	390	2	AH0260	conserved hypotet	525	6	2.8	450	2	AG0222	tailless (tll) pro
453	6	2.8	390	2	F81393	probable altronate	526	6	2.8	452	2	B47265	tailless (tll) pro
454	6	2.8	392	2	H71520	probable hch trans	527	6	2.8	452	2	A35602	tailless (tll) pro
455	6	2.8	392	2	F81676	heat shock gene re	528	6	2.8	453	2	A96688	hypothetical prote
456	6	2.8	393	2	AH3109	MPS permease [suga	529	6	2.8	454	1	TVPTAR	thyroid hormone re
457	6	2.8	396	2	F69813	multidrug-efflux t	530	6	2.8	454	2	B71914	alpha (1,3)-fucosy
458	6	2.8	397	2	T36819	hypothetical prote	531	6	2.8	454	2	D85020	hypothetical prote
459	6	2.8	397	2	AD3403	general L-amino ac	532	6	2.8	455	2	AB0909	serine protease (E
460	6	2.8	398	2	B70752	hypothetical prote	533	6	2.8	455	2	C91142	serine endoprotei
461	6	2.8	400	2	T05629	hypothetical prote	534	6	2.8	455	2	F85987	serine endoprotei
462	6	2.8	404	2	H87106	probable integral	535	6	2.8	455	2	JC6051	trypsin-like prote
463	6	2.8	404	2	AG2174	hypothetical prote	536	6	2.8	455	2	H84955	UDP-N-acetylmuram
464	6	2.8	407	2	AB2904	argininosuccinate	537	6	2.8	455	2	D83460	probable amino aci
465	6	2.8	407	2	A11159	flagellar biosynth	538	6	2.8	457	2	D90067	hypothetical prote
466	6	2.8	407	2	A11518	flagellar biosynth	539	6	2.8	457	2	AF2975	aminotransferase,
467	6	2.8	408	2	H87264	argininosuccinate	540	6	2.8	457	2	E98307	probable aminotran

541	6	2.8	458	2	AD2437	hypothetical prote	614	2	T42402	importin alpha 1 -
542	6	2.8	459	2	A39932	hypothetical prote	615	2	A69759	1-pyrroline-5-carb
543	6	2.8	460	2	D97679	argininosuccinate	616	6	F88618	protein W06F12.2 [
544	6	2.8	461	2	S69046	hypothetical prote	617	6	D37831	phenol 2-monooxyge
545	6	2.8	462	2	T30073	hypothetical prote	618	6	T10927	3C3.18c protein
546	6	2.8	463	2	A72779	hypothetical prote	619	6	G87343	cytochrome d ubiqu
547	6	2.8	464	1	P2ML13	L2 protein - human	620	6	C70776	probable export pr
548	6	2.8	465	2	S74905	hypothetical prote	621	6	T14752	microphthalmia-ass
549	6	2.8	466	2	A30306	probable amino aci	622	6	T36501	probable serine/th
550	6	2.8	467	2	T04540	adenylosuccinate 1	623	6	T24144	hypothetical prote
551	6	2.8	468	2	B69967	Na+/H+-exchanging	624	6	S42727	translation initia
552	6	2.8	470	2	T22785	hypothetical prote	625	6	S76810	probable NADH2 deh
553	6	2.8	472	1	YKXUM	citrate (tsi)-synth	626	6	S44982	flagellin - Shigel
554	6	2.8	473	2	H87238	pyridine transhydr	627	6	G83173	GMP synthase PA376
555	6	2.8	474	2	I50420	nonerythroid alpha	628	6	T07082	lycopene epsilon-c
556	6	2.8	475	2	G84312	glycine dehydrogen	629	6	S62439	hypothetical serin
557	6	2.8	476	2	B27671	spectrin alpha cha	630	6	E64106	2-isopropylmalate
558	6	2.8	477	2	A27671	spectrin alpha cha	631	6	T38326	serine threonine p
559	6	2.8	478	2	C64601	fucosyltransferase	632	6	A57173	oculocutaneous alb
560	6	2.8	479	2	T40330	hypothetical prote	633	6	AD0726	conserved hypothet
561	6	2.8	480	2	G90514	nadh oxidase (nox)	634	6	JS0304	developmental cont
562	6	2.8	481	2	H71084	hypothetical prote	635	6	T41384	hypothetical prote
563	6	2.8	482	2	D87290	conserved hypothet	636	6	F0MVND	gag polyprotein -
564	6	2.8	483	2	B33501	myosin heavy chain	637	6	H64241	arginine-trNA liga
565	6	2.8	484	2	S3501	RNA polymerase sig	638	6	G69875	hypothetical prote
566	6	2.8	485	2	F82065	probable exported	639	6	E71503	probable adp/atp t
567	6	2.8	486	2	AD0818	hypothetical prote	640	6	T48811	hypothetical prote
568	6	2.8	487	2	H83104	homeotic protein H	641	6	A55146	guanine nucleotide
569	6	2.8	488	2	A55180	serine-trNA ligase	642	6	T37516	major facilitator
570	6	2.8	489	2	T03949	flagellin - Salmon	643	6	S52489	choline oxidase (E
571	6	2.8	490	2	S09637	flagellin - Salmon	644	6	AH0098	probable methyl-ac
572	6	2.8	491	2	S69027	ammonium transport	645	6	JC4073	Tcp-1 containing c
573	6	2.8	492	2	S06907	thyroid hormone re	646	6	T05738	probable transcrip
574	6	2.8	493	2	I57696	c-erba-alpha-2-rel	647	6	B97346	oligopeptide ABC t
575	6	2.8	494	2	D71510	probable oligopept	648	6	T86516	fructose-6-P phosp
576	6	2.8	495	2	G81668	peptide ABC transp	649	6	A72106	pyrophosphate-fruc
577	6	2.8	496	2	A82294	probable carbon st	650	6	T24812	hypothetical prote
578	6	2.8	497	2	C89778	hypothetical prote	651	6	T23755	hypothetical prote
579	6	2.8	498	2	S43745	phosphatidylinosit	652	6	S51892	probable membrane
580	6	2.8	499	2	F75342	IMP dehydrogenase	653	6	T16696	hypothetical prote
581	6	2.8	500	2	T06332	dihydrolipoamide d	654	6	T43071	activation/secreti
582	6	2.8	501	2	A45856	hypothetical prote	655	6	S38035	probable serine/th
583	6	2.8	502	2	A98151	dipeptide transpor	656	6	T16589	hypothetical prote
584	6	2.8	503	2	AC3137	hypothetical prote	657	6	H82077	type IV pilus asse
585	6	2.8	504	2	S33193	phase-1 flagellin	658	6	T26242	hypothetical prote
586	6	2.8	505	2	S33190	phase-1 flagellin	659	6	T51348	RNA helicase RH25
587	6	2.8	506	2	S33188	phase-1 flagellin	660	6	T26243	hypothetical prote
588	6	2.8	507	2	S33187	phase-1 flagellin	661	6	S57812	leucyl aminopeptid
589	6	2.8	508	2	S33191	phase-1 flagellin	662	6	S74578	probable flavoprot
590	6	2.8	509	2	S33194	phase-1 flagellin	663	6	T43485	hypothetical prote
591	6	2.8	510	2	S33186	phase-1 flagellin	664	6	E70455	sulfur oxidation p
592	6	2.8	511	2	S33189	phase-1 flagellin	665	6	A96523	hypothetical prote
593	6	2.8	512	2	A3286	acetyl-CoA C-acety	666	6	H97105	carbon starvation
594	6	2.8	513	1	S38534	cytochrome P450 76	667	6	H64594	multidrug resistan
595	6	2.8	514	2	E64247	phosphoglycerate m	668	6	T51747	RNA helicase RH26
596	6	2.8	515	2	S33185	phase-1 flagellin	669	6	AF3490	DNA-directed DNA p
597	6	2.8	516	2	S33192	phase-1 flagellin	670	6	H87503	phosphogluconate d
598	6	2.8	517	2	T50398	hypothetical serin	671	6	B95950	probable two-compo
599	6	2.8	518	2	F96033	probable sugar upt	672	6	AD2590	two component sens
600	6	2.8	519	2	D98330	hypothetical prote	673	6	T06632	hypothetical prote
601	6	2.8	520	2	A12952	hypothetical prote	674	6	AG0227	exonuclease ABC c
602	6	2.8	521	1	O4CHC7	steroid 17alpha-mo	675	6	PN0012	mucin 4, tracheal
603	6	2.8	522	2	A53465	phase 1 flagellin	676	6	S65213	hypothetical prote
604	6	2.8	523	2	T01937	hypothetical prote	677	6	S06977	nlf-specific regul
605	6	2.8	524	2	A32225	nerve growth facto	678	6	D64714	cell division prot
606	6	2.8	525	2	C95282	probable ABC trans	679	6	T39758	proline-serine ric
607	6	2.8	526	2	C70624	probable two compo	680	6	S10450	myosin heavy chain
608	6	2.8	527	2	T45952	hypothetical prote	681	6	T47874	scarecrow-like pro
609	6	2.8	528	2	S13899	hypothetical prote	682	6	W1WL81	El protein - rhesu
610	6	2.8	529	2	S10527	endoglucanase B pr	683	6	G90570	hypothetical prote
611	6	2.8	530	1	A55407	IMP dehydrogenase	684	6	H82573	exonuclease ABC s
612	6	2.8	531	2	A05029	protochlorophyllid	685	6	T26064	hypothetical prote
613	6	2.8	532	2	G81298	probable periplasm	686	6	B42603	beta-glucoside-ape

687	6	2.8	635	2	JC5896	killer cell inhibi	760	6	2.8	774	2	B84031	ATP-dependent prot
688	6	2.8	637	2	A54000	sodium/phosphate c	761	6	2.8	774	2	A13372	malate dehydrogena
689	6	2.8	638	2	A48189	sodium/phosphate c	762	6	2.8	776	2	A46583	neuroendocrine-spe
690	6	2.8	639	2	B35816	transcription regu	763	6	2.8	783	2	B86254	hypothetical prote
691	6	2.8	640	2	B48189	sodium/phosphate c	764	6	2.8	787	2	E71537	probable 60kda inn
692	6	2.8	642	2	C96586	hypothetical prote	765	6	2.8	794	2	I58376	hypothetical prote
693	6	2.8	646	2	H71378	conserved hypotet	766	6	2.8	801	1	T52538	1-phosphatidylinos
694	6	2.8	646	2	A23409	ABC transporter AT	767	6	2.8	806	2	G84863	hypothetical prote
695	6	2.8	649	1	B37953	transcription regu	768	6	2.8	815	2	A71700	phenylalanine-tRNA
696	6	2.8	649	2	A35816	transcription regu	769	6	2.8	817	2	A48721	titin, muscle - ch
697	6	2.8	649	2	F83779	iron (III) dicitra	770	6	2.8	820	2	H86246	hypothetical prote
698	6	2.8	650	2	B81190	hypothetical prote	771	6	2.8	825	2	AC0039	glycerol-3-phospha
699	6	2.8	652	2	T16582	hypothetical prote	772	6	2.8	827	2	S25949	gene coxII intron
700	6	2.8	656	2	E97372	probable two-compo	773	6	2.8	829	2	AG0869	probable outer mem
701	6	2.8	661	1	A69048	ferrous iron trans	774	6	2.8	832	2	T49494	condensin complex
702	6	2.8	663	2	D96549	protein hypotetic	775	6	2.8	833	2	T02153	protein kinase hom
703	6	2.8	664	2	PC4002	phosphatidylinosit	776	6	2.8	834	2	T41568	argonaute-like pro
704	6	2.8	668	2	B96999	methyl-accepting c	777	6	2.8	835	2	T34770	probable protein p
705	6	2.8	674	2	T23235	hypothetical prote	778	6	2.8	838	2	S28911	gene DN10 protein
706	6	2.8	677	2	G84614	hypothetical prote	779	6	2.8	838	2	I45557	eyeless, long form
707	6	2.8	677	2	S23296	collagen alpha 2(I	780	6	2.8	839	2	S07226	RNA replicase 2a -
708	6	2.8	680	2	T25832	hypothetical prote	781	6	2.8	841	2	JC5894	killer cell inhibi
709	6	2.8	680	2	JC5895	killer cell inhibi	782	6	2.8	843	2	T06068	probable proton pu
710	6	2.8	681	2	F69295	acetyl-CoA synthet	783	6	2.8	843	2	H72204	pullulanase - Ther
711	6	2.8	681	2	S62390	zinc finger protei	784	6	2.8	843	2	S53947	hypothetical prote
712	6	2.8	685	2	G88733	protein F32E10.4 l	785	6	2.8	848	4	A44282	retrovirus-related
713	6	2.8	690	2	G84638	hypothetical prote	786	6	2.8	857	2	A82290	clpB protein VC071
714	6	2.8	695	2	I54325	gene XE7 protein -	787	6	2.8	858	2	S56205	probable membrane
715	6	2.8	698	1	S31630	NAD+-protein ADP-r	788	6	2.8	859	2	S69700	hypothetical prote
716	6	2.8	698	1	S31714	NAD+-protein ADP-r	789	6	2.8	860	2	T35971	conserved hypotet
717	6	2.8	698	2	T32840	hypothetical prote	790	6	2.8	864	2	T30441	probable capsid-as
718	6	2.8	701	2	C83052	polyribonucleotide	791	6	2.8	868	2	T43423	probable replicati
719	6	2.8	703	2	H86349	protein F8K7.9 [im	792	6	2.8	879	2	S64755	hypothetical prote
720	6	2.8	703	2	S40710	hypothetical prote	793	6	2.8	883	2	S04722	puff 74E protein -
721	6	2.8	707	2	T22127	hypothetical prote	794	6	2.8	887	2	AG2806	alanyl-tRNA synthet
722	6	2.8	711	2	C40046	antibiotic transpo	795	6	2.8	890	2	A97750	DNA mismatch repai
723	6	2.8	716	2	S45262	NF-AT component -	796	6	2.8	891	2	T30812	ubiquitin-protein
724	6	2.8	718	2	B81058	guanosine-3',5'-bi	797	6	2.8	892	2	T50339	miss protein limpo
725	6	2.8	718	2	T29708	hypothetical prote	798	6	2.8	893	2	D81989	hypothetical prote
726	6	2.8	718	2	JC5805	transcription fact	799	6	2.8	897	2	S05050	SIN1-associated pr
727	6	2.8	720	2	T43327	glucuronate transpor	800	6	2.8	900	2	T07585	alanyl-tRNA synthet
728	6	2.8	722	2	D71607	VPS45-like protein	801	6	2.8	903	2	F00358	hypothetical prote
729	6	2.8	725	2	B81819	guanosine-3',5'-bi	802	6	2.8	916	2	T35680	probable regulator
730	6	2.8	725	2	T03514	probable secretion	803	6	2.8	917	2	S26365	surface-layer prot
731	6	2.8	727	2	S18193	autoantigen NOR-90	804	6	2.8	920	2	S53961	hypothetical prote
732	6	2.8	727	2	JC5113	ribosomal transcri	805	6	2.8	925	2	T33732	probable exinucle
733	6	2.8	727	2	B40439	UBF transcription	806	6	2.8	928	1	S38001	probable serine/th
734	6	2.8	729	2	I54501	interferon gamma-i	807	6	2.8	928	2	C81265	probable lipoprote
735	6	2.8	730	2	A75486	hypothetical prote	808	6	2.8	931	2	A49737	dipeptidyl aminope
736	6	2.8	734	2	T04876	hypothetical prote	809	6	2.8	945	2	JN0901	endopeptidase clp
737	6	2.8	737	2	T02178	hypothetical prote	810	6	2.8	946	2	T16297	hypothetical prote
738	6	2.8	738	2	T19938	hypothetical prote	811	6	2.8	948	2	A57640	retinoblastoma bin
739	6	2.8	745	2	T44549	hypothetical prote	812	6	2.8	953	2	A86351	hypothetical prote
740	6	2.8	746	2	A84800	hypothetical prote	813	6	2.8	956	2	S64449	centromere-binding
741	6	2.8	747	2	T39744	conserved hypotet	814	6	2.8	958	2	S73012	polyketide synthas
742	6	2.8	750	2	S34683	hypothetical prote	815	6	2.8	962	2	S03818	carboxymethylcellu
743	6	2.8	754	2	S61113	YrA6 protein - yea	816	6	2.8	963	2	T09478	ubiquitin thiolest
744	6	2.8	754	2	A56619	female sterile hom	817	6	2.8	967	2	F87678	DNA polymerase I [
745	6	2.8	756	2	T20109	hypothetical prote	818	6	2.8	967	2	T15680	hypothetical prote
746	6	2.8	757	2	C32052	FixI protein - Rhi	819	6	2.8	976	2	S57725	respiration defici
747	6	2.8	757	2	C95344	FixII copper trans	820	6	2.8	978	2	D81411	probable lipoprote
748	6	2.8	757	2	T51428	hypothetical prote	821	6	2.8	983	2	T19874	hypothetical prote
749	6	2.8	760	2	D71445	hypothetical prote	822	6	2.8	985	2	B84489	hypothetical prote
750	6	2.8	764	2	S09318	transcription fact	823	6	2.8	986	2	E90596	restriction-modifi
751	6	2.8	764	2	JC5112	ribosomal transcri	824	6	2.8	986	2	S49394	HsdRI protein - My
752	6	2.8	764	2	A40439	UBF transcription	825	6	2.8	986	2	H90565	restriction modifi
753	6	2.8	765	2	S70962	regulatory protein	826	6	2.8	992	2	G70950	hypothetical prote
754	6	2.8	765	2	S22314	transcription fact	827	6	2.8	992	2	T46337	hypothetical prote
755	6	2.8	771	2	G71409	probable replicati	828	6	2.8	1005	2	T12546	hypothetical prote
756	6	2.8	772	2	D91195	hypothetical prote	829	6	2.8	1005	2	JC5799	probable adhesin 2
757	6	2.8	772	2	E86042	hypothetical prote	830	6	2.8	1018	2	H85611	alpha-D-mannosidas
758	6	2.8	772	2	B65167	hypothetical 88.1	831	6	2.8	1018	2	T30853	antigenic heat-sta
759	6	2.8	773	2	A46627	carnitine palmitoy	832	6	2.8	1020	2	E86165	FltK9.2 protein -



833 2.8 1026 2 C97783 cell surface antigen  
834 2.8 1030 2 A32612 spectrin alpha chain  
835 2.8 1035 1 GNPFG1 HIV-1 retropepsin  
836 2.8 1039 2 G83748 alpha-mannosidase  
837 2.8 1051 2 A38373 ubiquitin-protein  
838 2.8 1061 2 S75508 acriflavin resista  
839 2.8 1063 2 D86731 hypothetical prote  
840 2.8 1075 2 T45570 kinesin-like prote  
841 2.8 1078 2 T18352 protein p120 - Myc  
842 2.8 1085 2 E70834 probable regulator  
843 2.8 1086 2 JC7736 C3G protein, long  
844 2.8 1091 2 G84964 hypothetical prote  
845 2.8 1113 2 T26954 hypothetical prote  
846 2.8 1123 2 A39962 kinase-related tra  
847 2.8 1129 2 T19779 hypothetical prote  
848 2.8 1130 1 TVHUA protein-tyrosine k  
849 2.8 1138 2 E71615 probable amine tra  
850 2.8 1146 2 S84402 probable transcript  
851 2.8 1150 1 A55289 kinesin-like prote  
852 2.8 1179 2 H82706 hypothetical prote  
853 2.8 1195 2 S76592 5-methyltetrahydro  
854 2.8 1195 2 C87691 hypothetical prote  
855 2.8 1202 2 T17197 adenylate cyclase  
856 2.8 1203 2 T17415 mycelial surface a  
857 2.8 1209 2 T13153 brahma associated  
858 2.8 1212 2 T42387 histocompatibility  
859 2.8 1214 2 JC2069 zinc-finger protei  
860 2.8 1215 2 I52882 autoantigen - huma  
861 2.8 1217 2 T06007 hypothetical prote  
862 2.8 1237 2 A54080 protein-tyrosine-p  
863 2.8 1243 2 S60138 sex factor aggrega  
864 2.8 1258 2 T29041 hypothetical prote  
865 2.8 1263 2 T15496 hypothetical prote  
866 2.8 1280 2 A31981 hypothetical prote  
867 2.8 1293 1 YGCECF enterobactin synth  
868 2.8 1293 2 E85557 enterobactin synth  
869 2.8 1293 2 A30707 enterobactin synth  
870 2.8 1294 2 AF0574 enterobactin synth  
871 2.8 1314 2 S19488 probable membrane  
872 2.8 1319 2 S55598 tegument protein 0  
873 2.8 1321 2 A11592 phage protein homo  
874 2.8 1325 2 T14790 hypothetical prote  
875 2.8 1347 2 T30909 endo-1,4-beta-xyla  
876 2.8 1353 2 T19691 hypothetical prote  
877 2.8 1392 2 A43336 microtubule-vesicl  
878 2.8 1398 2 T20434 hypothetical prote  
879 2.8 1400 1 I38185 protein-tyrosine k  
880 2.8 1413 2 T26467 hypothetical prote  
881 2.8 1417 2 AG2137 hypothetical prote  
882 2.8 1426 2 T30567 ATP-binding casset  
883 2.8 1427 2 S22695 reelin - human  
884 2.8 1441 2 T00335 hypothetical prote  
885 2.8 1494 2 E89447 protein F57C12.4 [i  
886 2.8 1496 2 AH0447 insecticidal toxin  
887 2.8 1518 2 T44811 glucosyltransferase  
888 2.8 1560 2 T42727 proliferation pote  
889 2.8 1567 2 T00568 hypothetical prote  
890 2.8 1572 2 T00027 brain-specific ang  
891 2.8 1575 2 S68448 synaptotagmin, 170K  
892 2.8 1596 2 A35927 190K DNA-binding p  
893 2.8 1607 2 T43212 insulin-like growt  
894 2.8 1615 2 T06510 ras-responsive ele  
895 2.8 1623 2 T01369 ABC transporter At  
896 2.8 1671 2 S71628 sensory transducti  
897 2.8 1673 2 I50806 complement compone  
898 2.8 1677 2 T43021 vitellogenin precu  
899 2.8 1734 2 A54602 microtubule-associ  
900 2.8 1759 2 T03725 replicase polyprot  
901 2.8 1847 2 T28969 hypothetical prote  
902 2.8 1871 2 A87204 polyketide synthas  
903 2.8 1896 2 T01490 hypothetical prote  
904 2.8 1906 2 AD2443 smooth muscle myos  
905 2.8 1938 2 JC5421

906 2.8 1972 1 A41604 myosin heavy chain  
907 2.8 1972 2 JC5420 smooth muscle myos  
908 2.8 1993 2 T30902 sodium channel SCA  
909 2.8 2104 2 T38774 myosin-3 heavy cha  
910 2.8 2109 1 ZLVN genome polyprotein  
911 2.8 2150 1 GNNYH2 genome polyprotein  
912 2.8 2157 1 GNNY1B genome polyprotein  
913 2.8 2205 2 T08615 aggregation factor  
914 2.8 2228 2 T14029 variant-specific s  
915 2.8 2321 2 S78549 notch3 protein - h  
916 2.8 2401 2 T28676 rhoptry protein - h  
917 2.8 2422 2 T18201 fatty-acid synthas  
918 2.8 2472 2 A35715 fodrin alpha chain  
919 2.8 2477 1 SJCHA spectrin alpha cha  
920 2.8 2505 1 XYRTFA enoyl-[acyl-carrie  
921 2.8 2512 2 E70751 probable nrp prote  
922 2.8 2515 2 A41519 posterior-group pr  
923 2.8 2517 2 S58380 probable RNA-direc  
924 2.8 2535 2 AC0304 probable hemolysin  
925 2.8 2594 2 A35774 kinase-related pro  
926 2.8 2606 2 T24157 hypothetical prote  
927 2.8 2783 2 T34416 hypothetical prote  
928 2.8 2843 1 RBHUAP adenomatous polypo  
929 2.8 2845 2 I49505 adenomatous polypo  
930 2.8 3005 2 T08841 polypeptide - dour  
931 2.8 3010 1 GNVVTV genome polyprotein  
932 2.8 3010 1 S18030 genome polyprotein  
933 2.8 3169 2 T00296 toxin B - Escheric  
934 2.8 3187 2 JC5837 364K Golgi complex  
935 2.8 3588 2 I40485 surfactin syntheta  
936 2.8 3600 2 D86161 F1003.12 protein -  
937 2.8 3828 2 T13857 trithorax protein  
938 2.8 4077 2 T17484 hypothetical prote  
939 2.8 4351 2 T00252 MEGF1 protein - ra  
940 2.8 4377 2 A55575 ankyrin 3, long sp  
941 2.8 5627 2 C83339 hypothetical prote  
942 2.8 10223 2 T30225 polyketide synthas  
943 2.8 26926 1 I38344 titin, cardiac mus

## ALIGNMENTS

## RESULT 1

T46572  
probable UDP-glucuronic acid epimerase (EC 5.1.3.-) [imported] - Sinorhizobium meliloti  
C:Species: Sinorhizobium meliloti  
C:Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 09-Jul-2004  
C:Accession: T46572  
R:Kereszt, A.; Kiss, E.; Reuhs, B.L.; Carlson, R.W.; Kondorosi, A.; Putnoky, P.  
J. Bacteriol. 180, 5426-5431, 1998  
A:Title: Novel rkp gene clusters of Sinorhizobium meliloti involved in capsular polysac  
A:Reference number: 223086; MUID:98440435; PMID:9765575  
A:Accession: T46572  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-341 <KER>  
A:Cross-references: UNIPROT:O54067; EMBL:AJ222661; NID:g2959982; PIDN:CAA10917.1; PID:g2  
A:Experimental source: strain 41  
C:Genetics:  
A:Note: lpsL  
C:Function:  
A:Description: required for the synthesis of rhizobial capsular polysaccharide [validate  
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology  
C:Keywords: isomerase

Query Match 3.7%; Score 8; DB 2; Length 341;

Best Local Similarity 100.0%; Pred. No. 3.6;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 161 VGSNNMLE 168

Db 105 VGSNNMLE 112

```
RESULT 2
H72606
hypothetical protein APE1319 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H72606
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahashi, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6. 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-413 <KAW>
A;Cross-references: UNIPROT:Q9YCD8; DDBJ:AP000061; NID:G5104821; PIDN:BA80310.1; PID:cl
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE1319

Query Match 3.7%; Score 8; DB 2; Length 413;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSA 101
Db 12 LASSLSA 19

RESULT 3
T06576
probable protein kinase TCRR2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06576
R;Hackett, R.W.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z15770
A;Accession: T06576
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-982 <HAC>
A;Cross-references: UNIPROT:O65833; EMBL:AJ005077; NID:e1296722; PIDN:CAA06334.1; PID:cl
A;Experimental source: cultivar Ailsa Craig
C;Genetics:
A;Gene: TCRR2

Query Match 3.7%; Score 8; DB 2; Length 982;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 ASSLSAS 102
Db 30 ASSLSAS 37

RESULT 4
T17230
hypothetical protein DKFPz434E066.1 - human
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17230
R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18722
A;Accession: T17230
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-993 <KOE>
A;Cross-references: UNIPROT:Q9UES6; EMBL:AL117432
A;Experimental source: adult testis; clone DKFPz434E066
```

```
C;Genetics:
A;Note: DKFPz434E066.1

Query Match 3.7%; Score 8; DB 2; Length 993;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 ALASSLS 100
Db 7 ALASSLS 14

RESULT 5
T39219
atp-binding cassette transporter abc1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39219
R;McDougall, R.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21836
A;Accession: T39219
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1427 <MCD>
A;Cross-references: UNIPROT:Q92337; EMBL:Z99262; PIDN:CAB16410.1; GSPDB:GN00066; SPDB:SPJ
A;Experimental source: strain 972h-; cosmid c9E9
C;Genetics:
A;Gene: SPDB:SPAC9E9.12c
A;Map position: 1
A;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1427;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLD 75
Db 1391 KVLVLD 1398

RESULT 6
D86428
glutathione S-conjugate transporting ATPase (AtMRP1) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D86428
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86428
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1622 <STO>
A;Cross-references: UNIPROT:Q9C8G9; GB:AE005172; NID:g11055814; PIDN:AAG28284.1; GSPDB:GN
C;Genetics:
A;Map position: 1
A;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 3.7%; Score 8; DB 2; Length 1622;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 68 KVLVLD 75
```

Db 1440 KVLVDSG 1447

## RESULT 7

Tl3612

hypothetical protein 8D8.1 - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 09-Jul-2004

C:Accession: Tl3612

R:Papagiannakis, G.; Spanos, L.; Cox, S.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.

A:Reference number: Z17695

A:Accession: Tl3612

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2118 <PAP>

A:Cross-references: UNIPROT:O76904; EMBL:AL022018; PIDN:CAAL17682.1

C:Genetics:

A:Cross-references: FlyBase:FBgn0024367

A:Introns: 47/3; 726/3; 770/1; 813/3; 1404/1; 1473/3

A:Note: EG-8D8.1

C:Superfamily: Drosophila hypothetical protein EG\_8D8.1

## Query Match

Best Local Similarity 3.7%; Score 8; DB 2; Length 2118;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSLSSASA 103

|||||

Db 76 SSLSSASA 83

## RESULT 8

E72509

probable non specific lipid-transfer protein APE2051 - Aeropyrum pernix (strain Kl)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: E72509

R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: E72509

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-116 <KAW>

A:Cross-references: UNIPROT:Q9YA88; DDBJ:AP000063; NID:G5105654; PIDN:BAA81061.1; PID:dl

A:Experimental source: strain Kl

C:Genetics:

A:Gene: APE2051

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 116;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 96 SSLSSAS 102

|||||

Db 39 SSLSSAS 45

## RESULT 9

B72531

hypothetical protein APE2222 - Aeropyrum pernix (strain Kl)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004

C:Accession: B72531

R:Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: B72531

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-130 <KAW>

A:Cross-references: UNIPROT:Q9Y9R6; DDBJ:AP000063; NID:G5105654; PIDN:BAA81234.1; PID:dl

A:Experimental source: strain Kl

C:Genetics:

A:Gene: APE2222

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 130;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 LSSASAE 104

|||||

Db 45 LSSASAE 51

## RESULT 10

F96779

probable ribosomal protein S9 F9E10.17 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: F96779

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96779

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-132 <STO>

A:Cross-references: UNIPROT:Q9C9P6; GB:AEO05173; NID:G6646766; PIDN:AAF21078.1; GSPDB:GN

C:Genetics:

A:Gene: F9E10.17

A:Map position: 1

C:Superfamily: ribosomal protein S9/S16

## Query Match

Best Local Similarity 3.2%; Score 7; DB 2; Length 132;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 94 LASSLSS 100

|||||

Db 7 LASSLSS 13

## RESULT 11

F71189

hypothetical protein PH1790 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004

C:Accession: F71189

R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: F71189

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-133 <KAW>

A:Cross-references: UNIPROT:O59454; GB:AP000007; NID:G3236134; PIDN:BAA30909.1; PID:G325

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A;Gene: PHI790

Query Match 3.2%; Score 7; DB 2; Length 133;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 SSLSSAS 102  
|||||  
Db 68 SSLSSAS 74

#### RESULT 12

E64375  
hypothetical protein MJ0605 - Methanococcus jannaschii  
C;Species: Methanococcus jannaschii  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: E64375  
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Son, J.D.; Sadow, P.W.; 1996  
Science 273, 1058-1073, 1996  
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.R.; Olsen, G.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.; Bult, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Reich, C.I.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.; Son, J.D.; Sadow, P.W.; 1996  
Science 273, 1058-1073, 1996  
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A;Reference number: A64300; MUID:96337999; PMID:8688087  
A;Accession: E64375  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-134 <BUL>  
A;Cross-references: UNIPROT:Q58022; GB:U67508; GB:L77117; NID:g1591300; PIDN:AAB98599.1;  
C;Genetics:  
A;Map position: REV535846-535442  
A;Start codon: GTG

Query Match 3.2%; Score 7; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 KNLNPKK 59  
|||||  
Db 58 KNLNPKK 64

#### RESULT 13

JE0264  
cyclin I - human  
C;Species: Homo sapiens (man)  
C;Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
C;Accession: JE0264  
R;Zhu, X.; Naz, R.K.  
Biochem. Biophys. Res. Commun. 249, 56-60, 1998  
A;Title: Expression of a novel isoform of cyclin I in human testis.  
A;Reference number: JE0264; MUID:98381026; PMID:9705831  
A;Accession: JE0264  
A;Molecule type: mRNA  
A;Residues: 1-178 <ZHU>  
A;Cross-references: UNIPROT:Q14094  
C;Comment: This protein may have a physiological role in spermatogenesis and/or human spermatogenesis

Query Match 3.2%; Score 7; DB 2; Length 178;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 FALASSL 98  
|||||  
Db 66 FALASSL 72

#### RESULT 14

T49611  
hypothetical protein B3E4.240 [imported] - Neurospora crassa  
C;Species: Neurospora crassa  
C;Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C;Accession: T49611

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000  
A;Reference number: Z25022

A;Accession: T49611  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-185 <SCH>  
A;Cross-references: UNIPROT:Q9P5V8; EMBL:AL355931; GSPDB:GN00116; NCSP:B3E4.240  
A;Experimental source: BAC clone B3E4; strain OR74A  
C;Genetics:  
A;Gene: NCSP:B3E4.240  
A;Map position: 6

Query Match 3.2%; Score 7; DB 2; Length 185;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 97 SLSSASA 103  
|||||  
Db 34 SLSSASA 40

#### RESULT 15

T52450  
ribosomal protein S9 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 09-Jul-2004  
C;Accession: T52450  
R;Arimura, S.; Takusagawa, S.; Hatano, S.; Nakazono, M.; Hirai, A.; Teutsumi, N.; FEBS Lett. 450, 231-234, 1999  
A;Title: A novel plant nuclear gene encoding chloroplast ribosomal protein S9 has a transmembrane domain  
A;Reference number: Z26079  
A;Accession: T52450  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-208 <ARI>  
A;Cross-references: UNIPROT:Q9XJ27; EMBL:AB022676; PIDN:BAAG2396.1  
C;Genetics:  
A;Gene: rps9  
C;Superfamily: ribosomal protein S9/S16

Query Match 3.2%; Score 7; DB 2; Length 208;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 94 LASSLS 100  
|||||  
Db 7 LASSLS 13

Search completed: October 13, 2005, 18:55:46  
Job time : 37 secs